

STIC-Biotech/ChemLib

153748

mej

From: Hutzell, Paula  
Sent: Wednesday, May 18, 2005 7:07 AM  
To: Graser, Jennifer; STIC-Biotech/ChemLib  
Subject: RE: rush search

approved

RECEIVED  
MAY 18 2005  
(STIC)

-----Original Message-----

From: Graser, Jennifer  
Sent: Tuesday, May 17, 2005 4:48 PM  
To: Hutzell, Paula  
Subject: rush search  
Importance: High

Hi Paula,  
Could you please authorize this ~~rush~~ search for an amendment which is due?  
Thanks, Jennifer

-----  
STIC:  
Please search SEQ ID NO: 1 and 2 for Serial No. 10/650,123 in pending and commercial  
databases.

Thanks,  
Jennifer Graser  
REM 3B09 (mailbox 3C18)  
Art Unit 1645  
272-0858

Interference  
Search in  
Ex Office

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

*This Page Blank (uspto)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 13:06:08 ; Search time 7006 Seconds  
(without alignments)  
3631.029 Million cell updates/sec

Title: US-10-650-123-1  
Perfect score: 525  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
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2: gb.htg.\*  
3: gb.in.\*  
4: gb.on.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
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2	525	100.0	525 1	AF175682	Neisseria
3	525	100.0	525 1	AF175683	Neisseria
4	525	100.0	525 6	C0786532	Sequence
5	525	100.0	525 6	C0814512	Sequence
6	525	100.0	830 1	NMU52066	Neisseria m
7	525	100.0	830 6	AR167414	Sequence
8	521.8	99.4	525 1	AF175678	Neisseria
9	521.8	99.4	10057 1	AE002420	Neisseria
10	521.8	99.4	349980 6	AX044030	Sequence
11	518.6	98.8	850 1	NMU52068	Neisseria m
12	518.6	98.8	850 6	AR167416	Sequence
13	518.6	98.8	311321 1	NMA322491	Neisseria
14	517	98.5	525 1	AF175677	Neisseria
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ALIGNMENTS

RESULT 1	AF175680	Neisseria meningitidis strain M986 surface protein A (nspA) gene, complete cds.	525 bp	DNA	linear	BCT 06-SEP-1999
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DEFINITION	AF175680.1	GI:5825535				
ACCESSION	AF175680					
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
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JOURNAL						
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
AF175682
LOCUS
DEFINITION
Neisseria meningitidis strain NG6/88 surface protein A (nsa) gene,
complete cds.
ACCESSION
AF175682
VERSION
AF175682.1 GI:5825540
KEYWORDS
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
ORGANISM
1 (bases 1 to 525)
REFERENCE
AUTHORS
Moe,G.R., Tan,S. and Granoff,D.M.
TITLE
Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains
JOURNAL
Infect. Immun. (1999) In press
AUTHORS
Moe,G.R., Tan,S. and Granoff,D.M.
TITLE
Direct Submission
JOURNAL
Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
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RESULT 3
AF175683
LOCUS
DEFINITION
Neisseria meningitidis strain NG165 surface protein A (nsa) gene,
complete cds.
ACCESSION
AF175683
VERSION
AF175683.1 GI:5825542
KEYWORDS
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
ORGANISM
1 (bases 1 to 525)
REFERENCE
AUTHORS
Moe,G.R., Tan,S. and Granoff,D.M.
TITLE
Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains
JOURNAL
Infect. Immun. (1999) In press
AUTHORS
Moe,G.R., Tan,S. and Granoff,D.M.
TITLE
Direct Submission
JOURNAL
Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
FEATURES
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JOURNAL Submitted (04-AUG-1999) Children's Hospital Oakland Research Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

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ORIGIN

Query Match 100.0%; Score 525; DB 1; Length 525;  
Best Local Similarity 100.0%; Pred. No. 1.5e-96;  
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DEFINITION Sequence 1 from Patent WO2004019976.  
ACCESSION CQ786532  
VERSION CQ786532.1 GI:45721576  
KEYWORDS Neisseria meningitidis  
SOURCE Neisseria meningitidis  
ORGANISM

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
Neisseriaceae; Neisseria.

REFERENCE

AUTHORS Martin, D. and Rioux, S.  
TITLE Pharmaceutical liposomal compositions containing n. Meningitidis  
JOURNAL derived polypeptides or polynucleotides  
Patent: WO 2004019976-A 1 11-MAR-2004;  
SHIRE BIOCHEM, INC. (CA)

FEATURES

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VERSION CQ814512.1 GI:47603711  
KEYWORDS Neisseria meningitidis  
SOURCE Neisseria meningitidis  
ORGANISM Neisseria meningitidis  
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Neisseriaceae; Neisseria.  
REFERENCE 1  
AUTHORS Bismans, R., Bos, M., Denoel, P., Feron, C., Goraj, K., Poolman, J.,  
Tomassen, J. and Weynants, V.  
TITLE Refolding method  
JOURNAL Patent: WO 2004020452-A 8 11-MAR-2004;

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DEFINITION          Neisseria meningitidis outer membrane protein gene, complete cds.
ACCESSION            U52066
VERSION              U52066.1 GI:1518521
KEYWORDS
SOURCE               Neisseria meningitidis
ORGANISM             Neisseria meningitidis
Bacteria: Proteobacteria; Betaproteobacteria, Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 830)
Martin, D., Cadieux, N., Hamel, J. and Brodeur, B.R.
Highly conserved Neisseria meningitidis surface protein confers
protection against experimental infection
J. Exp. Med. 185 (7), 1173-1183 (1997)
97258610
PUBMED              9104804
2 (bases 1 to 830)
Plante, M., Cadieux, N., Rioux, C.R., Hamel, J., Brodeur, B.R. and
Martin, D.
Antigenic and molecular conservation of the gonococcal NspA protein
Infect. Immun. 67 (6), 2855-2861 (1999)
99270944
MEDLINE

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PUBMED              10338491
REFERENCE            3 (bases 1 to 830)
AUTHORS              Cadieux, N., Plante, M., Rioux, C.R., Hamel, J., Brodeur, B.R. and
                    Martin, D.
TITLE                Bactericidal and cross-protective activities of a monoclonal
                    antibody directed against Neisseria meningitidis NspA outer
                    membrane protein
JOURNAL              Infect. Immun. 67 (9), 4955-4959 (1999)
MEDLINE              99386904
PUBMED              10456958
REFERENCE            4 (bases 1 to 830)
AUTHORS              Martin, D.
TITLE                Direct Submission
JOURNAL              Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,
                    University Laval, Unite de Vaccinologie, Laboratoire et Service
                    d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACTGATTCCTTCCTCCCGCCCGCCGCACTGGCGGAA 60
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Db 503 AGCAAACTCTCATCGGCTCGGCTATTTGACGGCGTAAAGTATGCGCTTACCCGAAT 562
QY 421 GTGATTTGATGTCGGCTACGCTACAACTACGCAAGTCAAACTGTCAAAAC 480

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Db 623 GTCGCTTCGGCGAACTGTCGCTGGCGTGGCGGTCAAAATCTGA 667

RESULT 7

ARI67414

LOCUS

DEFINITION

Sequence 1 from patent US 6287574.

ACCESSION

ARI67414

VERSION

ARI67414.1 GI:17903193

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 830)

AUTHORS

Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.

TITLE

Proteinase K resistant surface protein of neisseria meningitidis

JOURNAL

Patent: US 6287574-A 1 11-SEP-2001;

FEATURES

Location/Qualifiers

source

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ORIGIN

Query Match 100.0%; Score 525; DB 6; Length 830;

Best Local Similarity 100.0%; Pred. No. 1.5e-96;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCACTGCGCACACTGATTCCTCGCTCTCCCGGCGCGCACTGCGGAA 60

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Qy 61 GCGCATCCGGCTTTACGTCACAGCGATCGGCACACGCAAGCTCAAGCTCTTTA 120

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ACCESSION

AF175678

VERSION

AF175678.1 GI:5825530

KEYWORDS

Neisseria meningitidis

SOURCE

Neisseria meningitidis

ORGANISM

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 525)

AUTHORS

Moe, G.R., Tan, S. and Granoff, D.M.

TITLE

Differences in Surface Expression of Neisserial Surface Protein A

JOURNAL

Infect. Immun. (1999) In press

REFERENCE

2 (bases 1 to 525)

AUTHORS

Moe, G.R., Tan, S. and Granoff, D.M.

TITLE

Direct Submission

JOURNAL

Submitted (04-AUG-1999) Children's Hospital Oakland Research

INSTITUTE, 747 Fifty-Second Street, Oakland, CA 94609, USA

FEATURES

Location/Qualifiers

source

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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 6.9e-96;

Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCACTTGCACACTGATTCCTCGCTCTCCCGGCGCGCACTGCGGAA 60

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Db 121 GGTTCGCAAGGCTTCAGCGCGGCACTCTCCGAGGCTACCGCATCAAGCACTCCGC 180

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RESULT 8

AF175678

LOCUS

DEFINITION

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complete cds.

525 bp DNA linear BCT 06-SEP-1999

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RESULT 9
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LOCUS
DEFINITION
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the complete genome.
ACCESSION
AE002420 AB002098
VERSION
AE002420.1 GI:7225876
KEYWORDS
SOURCE
Neisseria meningitidis MC58
ORGANISM
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 10057)
Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Qin, H., Vanathevan, J., Gill, J., Scarlato, V., Masignani, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Complete genome sequence of Neisseria meningitidis serogroup B
strain MC58
Science 287 (5459), 1809-1815 (2000)
20175755
10710307
REFERENCE
2 (bases 1 to 10057)
Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Qin, H., Vanathevan, J., Gill, J., Scarlato, V., Masignani, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Direct Submission
Submitted (17-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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RESULT 10
AX044030 349980 bp DNA linear PAT 24-NOV-2000
LOCUS
DEFINITION Sequence 109 from Patent WO0066791.
ACCESSION AX044030
VERSION AX044030.1 GI:11342914
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,
Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarlatti, M.,
Scarlato, V., Rappuoli, R., Frazer, C.M. and Grandi, G.
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 109 09-NOV-2000;
CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
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Best Local Similarity 99.6%; Pred. No. 4.7e-96;
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 11  
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 ACCESSION U52068  
 VERSION U52068.1 GI:1808966  
 SOURCE Neisseria meningitidis  
 ORGANISM Neisseria meningitidis  
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 Neisseriaceae; Neisseria.  
 1 (bases 1 to 850)  
 Martin, D.  
 Cadieux, N., Plante, M., Rioux, C.R., Hamel, J., Brodeur, B.R. and  
 Bactericidal and cross-protective activities of a monoclonal  
 antibody directed against Neisseria meningitidis NspA outer  
 membrane protein  
 Infect. Immun. 67 (9), 4955-4959 (1999)  
 JOURNAL MEDLINE 99386904  
 PUBMED 10456958  
 REFERENCE 2 (bases 1 to 850)  
 Martin, D.  
 Direct Submission  
 Submitted (22-MAR-1996) Denis Martin, Department of Microbiology,  
 University Laval, Unite de Vaccinologie, Laboratoire et Service  
 d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705  
 boul Laurier, Ste-Foy, Quebec G1V 4G2, Canada  
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 Db 268 GCGCATCGCGCTTTAGCTCCAGCCGATCCGACACGCAAGAAAGCTCAAGCTCTTTA 327  
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 Db 328 GGTTCCTGCAAAAGCTTCAGCCCGGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 387  
 QY 181 TTCGCGCTCGATTACACGCGCTACAAAACTATAAGCCGCCATCCACCGATTCAAACTT 240  
 Db 388 TTCGCGCTCGATTACACGCGCTACAAAACTATAAGCCGCCATCCACCGATTCAAACTT 447  
 QY 241 TACAGATCGCGCGCTCCGCGCATTTACGACTTCGACACCCCAATCGCCGTCACACCGTAT 300  
 Db 448 TACAGATCGCGCGCTCCGCGCATTTACGACTTCGACACCCCAATCGCCGTCACACCGTAT 507  
 QY 301 CTCGCGCGCGCTTGAGCTCTCAACCGCGCTCCGTCGACTTGGGCGGACGACAGCTTC 360  
 Db 508 CTCGCGCGCGCTTGAGCTCTCAACCGCGCTCCGTCGACTTGGGCGGACGACAGCTTC 567  
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 Db 568 AGCCAAACCTCAATCGCGCTTCGCGCTATTGACGGCGCTAAAGCTATGCCGTTACCCCGAAT 627  
 QY 421 GTCGATTGATGTCGCGCTACCGCTACAACTACATCGGCAAAAGTCAACTGTCAAAAC 480  
 Db 628 GTCGATTGATGTCGCGCTACCGCTACAACTACATCGGCAAAAGTCAACTGTCAAAAC 687  
 QY 481 GTCGTTCCGCGCAACTGTCGTCGCGTCCGCTCGCGCTCAAAATTCGA 525  
 Db 688 GTCGTTCCGCGCAACTGTCGTCGCGTCCGCTCGCGCTCAAAATTCGA 732  
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 LOCUS ARI67416 850 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 5 from patent US 6287574.  
 ACCESSION ARI67416  
 VERSION ARI67416.1 GI:17903195  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCES  
 1 (bases 1 to 850)  
 Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.  
 Proteinase K resistant surface protein of neisseria meningitidis  
 Patent: US 6287574-A 5 11-SEP-2001;  
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Qy      121 GGTTCGCAAAAGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACTCCGC 180
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Qy      181 TTCCGCGTCGATTACACGCGCTACAAAACCTATAAGCCCATCCACCGATTTCAACTT 240
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Qy      301 CTCGCGCGCGCTTGAGCTCAACCGCGCTCCGCTCGACTTGGGCGGCGAGCAGCTTC 360
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LOCUS Neisseria meningitidis serogroup A strain Z2491 complete genome;
DEFINITION segment 3/7.
ACCESSION AL162754 AL157959
VERSION AL162754.2 GI:7379424
KEYWORDS
SOURCE
ORGANISM Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 311321)
Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C.,
Klee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T.,
Davies, R.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N.,
Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K.,
Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M.,
Skellton, J., Whitehead, S., Spratt, B.G. and Barrall, B.G.
Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491
JOURNAL Nature 404 (6777), 502-506 (2000)
MEDLINE 2022556
PUBMED 10761919
REFERENCE 2 (bases 1 to 311321)
Parkhill, J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
Notes:
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World wide web.
(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
FEATURES
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/organism="Neisseria meningitidis Z2491"

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unknown, contains a probable N-terminal signal sequence
and lies within a region of unusually low GC content"
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742..1077
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742..1077
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protein, len: 336 bp; similar to C-termini of many ABC
transporters e.g. TR:O46973 (EMBL:U47048), mtfB,
Escherichia coli microcin transport protein (707 aa),
fasta scores; E(): 2.6e-19, 53.2% identity in 111 aa
overlap. Contains P800211 ABC transporters family
signature. NMA0686 may be the remainder of this
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868..912
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complement(1101..2327)
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/note="NMA0700, possible ribonuclease BN, len: 408 aa;
similar to SW:RBN_ECOLI (EMBL:L19201), rbn, Escherichia
coli ribonuclease BN (EC 3.1.1.-), fasta scores; E():
2.3e-28, 34.3% identity in 268 aa overlap. Longer than rbn
at the C-terminus. Also similar to TR:O85449
(EMBL:AF067083) Vitreoscilla sp. hypothetical protein (376
aa), fasta scores; E(): 0.45e-04 identity in 333 aa
overlap. Contains a region similar to NMA0677, fasta
scores; E(): 4.3e-08, 64.4% identity in 45 aa overlap.
Contains hydrophobic, possible membrane-spanning regions,
as does rbn"
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/label=DUS
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/pseudo
2486..2743
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wrbA, Escherichia coli Ttp repressor binding protein (197
aa), fasta scores; E(): 0.064, 29.3% identity in 82 aa
overlap. Also similar to part of TR:O85450 (EMBL:AF067083)
Vitreoscilla sp. Ttp repressor binding protein (fragment)
(124 aa), fasta scores; E(): 6.6e-14, 56.6% identity in 83
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2871..3530
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(EMBL:Z50189), exsB, Rhizobium meliloti putative regulator
of succinoglycan biosynthesis (not a transcriptional
regulator) (234 aa), fasta scores; E(): 3.1e-15, 32.7%
identity in 205 aa overlap. Also similar to many
bacterial hypothetical proteins e.g. SW:YBAX_HAEIN
(EMBL:U32798), Hili91, Haemophilus influenzae hypothetical
protein (196 aa), fasta scores; E(): 0.79.2% identity in
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4083..4505
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fasta scores; E(): 5.1e-32, 58.0% identity in 138 aa
overlap. Shows very weak similarity to eukaryotic
6-pyruvoyl-tetrahydropterin synthases e.g. SW:PTPS_RAT
(EMBL:M77850), pte, Rattus norvegicus 6-pyruvoyl
tetrahydrobiopterin synthase precursor (EC 4.6.1.10) (144
aa)
Query Match 98.8%; Score 518.6; DB 1; Length 311321;
Best Local Similarity 99.2%; Pred. No. 2.1e-95;
Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 ATGAAAAAGCACTTGCACACTGATTGCGCTTCCTTCCTCCGCGCGCACTGCGGAA 60
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AF175677
LOCUS
DEFINITION
Neisseria meningitidis strain BZ232 surface protein A (nspA) gene,
complete cds.
ACCESSION
AF175677
VERSION
AF175677.1 GI:5825528
KEYWORDS
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

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REFERENCE 1 (bases 1 to 525)
AUTHORS Moe,G.R., Tan,S. and Granoff,D.M.
TITLE Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains
JOURNAL Infect. Immun. (1999) In press
REFERENCE 2 (bases 1 to 525)
AUTHORS Moe,G.R., Tan,S. and Granoff,D.M.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
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ORIGIN
Query Match 98.5%; Score 517; DB 1; Length 525;
Best Local Similarity 99.0%; Pred. No. 6.5e-95;
Matches 520; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCACTTGCACACTGATTCGCTCGCTCCCGCGCGCGCACTGCGGAA 60
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ACCESSION AF175679
VERSION AF175679.1 GI:5825533
KEYWORDS Neisseria meningitidis
SOURCE Neisseria meningitidis
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 525)
AUTHORS Moe,G.R., Tan,S. and Granoff,D.M.
TITLE Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains
JOURNAL Infect. Immun. (1999) In press
REFERENCE 2 (bases 1 to 525)
AUTHORS Moe,G.R., Tan,S. and Granoff,D.M.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
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ORIGIN
Query Match 98.5%; Score 517; DB 1; Length 525;
Best Local Similarity 99.0%; Pred. No. 6.5e-95;
Matches 520; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGAAAAAGCACTTGCACACTGATTCGCTCGCTCCCGCGCGCGCACTGCGGAA 60
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Search completed: May 19, 2005, 17:22:51  
 Job time : 7013 secs

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2	525	100.0	525	12 ADL24351	Adl24351 N meningi
3	525	100.0	830	2 AAT39039	Aat39039 Proteinas
4	525	100.0	830	8 ACA64711	AcA64711 N. mening
5	525	100.0	830	10 ADF43315	Adf43315 N. mening
C 6	521.8	99.4	37668	3 AAA81490_14	Continuation (15 o
C 7	521.8	99.4	110000	3 AAR81490_06	Continuation (7 o
C 8	521.8	99.4	349980	3 AAF21608	Aaf21608 Neisseria
9	518.6	98.8	850	2 AAT39041	Aat39041 Proteinas
10	502.6	95.7	710	6 ABS67381	AbS67381 Neisseria
11	502.6	95.7	810	2 AAT39042	Aat39042 Proteinas
12	491.2	93.6	710	2 AAT39040	Aat39040 Proteinas
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C 15	368	70.1	486	10 ABZ38960	Abz38960 N. gonorr
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18	51.4	9.8	985	6 ABQ44817	Abq44817 Oligonuc
19	49.8	9.5	1919	12 ADM94375	Adm94375 Wheat ABC
20	49.2	9.4	86941	12 ADI39160	Adi39160 Streptomy

DR P-PSDB; ADL13428.

XX New refolded NspA protein, useful for preparing a composition for

PT diagnosing, treating or preventing infection caused by *Neisseria*

PT meningitidis or *Neisseria gonorrhoeae*.

XX Disclosure; Fig 3; 62pp; English.

XX The invention relates to an isolated refolded *Neisseria* surface protein

CC A (NspA) from *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The

CC invention also relates to the method of refolding an NspA protein; an

CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-  
 CC dimethyladecylammonio)propanesulphonate) for refolding an NspA protein; a

CC pharmaceutical composition comprising the refolded NspA protein; a

CC carrier and optionally one or more other *Neisseria* antigens; a method of

CC preventing or treating a *Neisseria* infection; an antibody immunospecific

CC for the NspA protein; and diagnosing a *Neisseria* infection. NspA has

CC characteristics which indicate that it is a potential vaccine candidate

CC for the development of subunit vaccines for the treatment of infections

CC caused by *Neisseria meningitidis* (meningococcus), which causes invasive

CC bacterial diseases such as bacteraemia and meningitis, or *Neisseria*

CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced

CC NspA could therefore be used to produce vaccine compositions and it could

CC also be used in the development of new antimicrobial agents, diagnostic

CC tests and in drug screening. However, recombinantly produced proteins are

CC frequently unable to adopt their biologically active conformations, and

CC yields may be very low due to mis-folding and aggregation of the protein.

CC The method of the invention provides an improved method for refolding the

CC NspA protein, and it is possible to increase the recovery of active

CC protein form partly purified inclusion bodies in amounts up to 100%

CC without the need for further purification. The refolded NspA protein is

CC useful for preparing a composition for diagnosing, treating or preventing

CC infection caused by *Neisseria meningitidis* or *Neisseria gonorrhoeae*. The

CC present sequence represents the NspA gene from *Neisseria meningitidis*

CC H44/76.

XX

SQ Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 12; Length 525;

Best Local Similarity 100.0%; Pred. No. 4.7e-125;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGGCACACTGATGGCTCTCCGGCCCGCGCACTGGCGGAA 60

DB 1 ATGAAAAAGCACTTGGCACACTGATGGCTCTCCGGCCCGCGCACTGGCGGAA 60

QY 61 GGCGCATCGGCTTTACGTCCAAAGCGATGGCGACACGCAAAAGCCTCAAGCTCTTTA 120

DB 61 GGCGCATCGGCTTTACGTCCAAAGCGATGGCGACACGCAAAAGCCTCAAGCTCTTTA 120

QY 121 GGTCTCTGCCAAGGCTTCAGCCCGCGCATCTCCGACGGCTACCGCATCAACGACCTCCGC 180

DB 121 GGTCTCTGCCAAGGCTTCAGCCCGCGCATCTCCGACGGCTACCGCATCAACGACCTCCGC 180

QY 181 TTGCGCGTGATTAACGGCGCTACAAAACTATAAAGCCCATTCACCGATTCAAACTT 240

DB 181 TTGCGCGTGATTAACGGCGCTACAAAACTATAAAGCCCATTCACCGATTCAAACTT 240

QY 241 TACAGCATCGGCGCTTCGCGCATTTACGACTTCGACACCCCAATCGCCGCTCAACCGTAT 300

DB 241 TACAGCATCGGCGCTTCGCGCATTTACGACTTCGACACCCCAATCGCCGCTCAACCGTAT 300

QY 301 CTCGGCGCGGCTTTAGACCTCAACCGCGCTTCGTCGACTTGGCGGCGACGACGCTTC 360

DB 301 CTCGGCGCGGCTTTAGACCTCAACCGCGCTTCGTCGACTTGGCGGCGACGACGCTTC 360

QY 361 AGCCAAACCTCATTCGGCGCTTCGCGGCTTGAACGGCGTAAAGTATGCCGTTACCCGGAAT 420

DB 361 AGCCAAACCTCATTCGGCGCTTCGCGGCTTGAACGGCGTAAAGTATGCCGTTACCCGGAAT 420

QY 421 GTCGATTTGGATGCGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 480

DB 421 GTCGATTTGGATGCGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAAC 480

QY 481 GTCCGTTCCGGCAACTGTCCGTCCGGCGTCCGCTCAAAATTCGA 525

DB 481 GTCCGTTCCGGCAACTGTCCGTCCGGCGTCCGCTCAAAATTCGA 525

RESULT 2

ADL24351

ID ADL24351 standard; DNA; 525 BP.

XX ADL24351;

AC ADL24351;

DT 03-JUN-2004 (first entry)

XX N meningitidis strain 608B NspA coding sequence.

DE ds; gene; NspA; vaccine; antibacterial; meningitis.

XX *Neisseria meningitidis*.

OS

EH Key Location/Qualifiers

FT CDS 1..525

FT /\*tag= a

FT /product= "NspA"

XX WO2004019976-A2.

PD 11-MAR-2004.

XX 29-AUG-2003; 2003WO-CA001452.

XX 30-AUG-2002; 2002US-0406980P.

XX (SHIR-) SHIRE BIOCHEM INC.

XX Martin D, Rioux S;

XX WPI; 2004-239123/22.

DR P-PSDB; ADL24352.

XX Composition comprising liposome associated with isolated polypeptide or

PT polynucleotide derived from *Neisseria meningitidis* strain 608B, or its

PT fragment or analog, useful for inducing an immune response against N.

PT meningitidis.

XX Claim 9; Fig 1; 79pp; English.

XX The present invention relates to a pharmaceutical composition comprising

CC a liposome associated with an isolated polypeptide derived from *Neisseria*

CC meningitidis strain 608B, where the polypeptide is the NspA protein. The

CC composition is useful for inducing an immune response against N.

CC meningitidis, for preventing and/or treating N. meningitidis infection

CC and for treating and/or preventing *Neisseria* infection chosen from N.

CC meningitidis, N. gonorrhoeae, N. lactamica and N. polysacchara. It is

CC useful for treatment or prophylaxis of meningitis and meningococemia, in

CC a host. The host is a mammal, preferably a human and more preferably an

CC adult human. The present sequence is the *Neisseria meningitidis* strain

CC 608B NspA coding sequence.

XX Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 525; DB 12; Length 525;

Best Local Similarity 100.0%; Pred. No. 4.7e-125;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGGCACACTGATGGCTCTCCGGCCCGCGCACTGGCGGAA 60

DB 1 ATGAAAAAGCACTTGGCACACTGATGGCTCTCCGGCCCGCGCACTGGCGGAA 60

QY 61 GGCGCATCGGCTTTACGTCCAAAGCGATGGCGACACGCAAAAGCCTCAAGCTCTTTA 120

DB 61 GGCGCATCGGCTTTACGTCCAAAGCGATGGCGACACGCAAAAGCCTCAAGCTCTTTA 120



QY 121 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 180  
 DB 121 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 180  
 QY 181 TTCGCGCTCGATTACACGCGCTACAAAACTATAAGCCCATCCACCGATTTCAACTT 240  
 DB 181 TTCGCGCTCGATTACACGCGCTACAAAACTATAAGCCCATCCACCGATTTCAACTT 240  
 QY 241 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCACAAACCGTAT 300  
 DB 241 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCACAAACCGTAT 300  
 QY 301 CTCGCGCGGCTTCAGCTTCACCGCGCTCCGCTCGAGCTGGGCGGAGGACGCTTC 360  
 DB 301 CTCGCGCGGCTTCAGCTTCACCGCGCTCCGCTCGAGCTGGGCGGAGGACGCTTC 360  
 QY 361 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 420  
 DB 361 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 420  
 QY 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480  
 DB 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480  
 QY 481 GTCGATTTGGGGAAGTGTCCGCTCGCGCTGCGCTCAAAATTCGA 525  
 DB 481 GTCGATTTGGGGAAGTGTCCGCTCGCGCTGCGCTCAAAATTCGA 525

RESULT 3

AT39039  
 ID AAT39039 standard; DNA; 830 BP.

AC AAT39039;  
 XX 16-OCT-2003 (revised)  
 DT 22-DEC-1996 (first entry)

Proteinase K resistant N. meningitidis 22 kD surface protein.

Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
 antibody; detection; probe; surface protein; ss.

Neisseria meningitidis; strain 608B.

Key	Location/Qualifiers
-10_signal	75..80
RBS	/tag= d
CDS	131..135
sig_peptide	/tag= e
mat_peptide	143..667
	/tag= a
	143..199
	/tag= b
	200..664
	/tag= c

W09629412-A1.

26-SEP-1996.

15-MAR-1996; 96WO-CA000157.

17-MAR-1995; 95US-00406362.

04-AUG-1995; 95US-0001983P.

(IAFB-) IAF BIO VAC INC.

Brodeur BR, Martin D, Hamel J, Rioux C;

WPI; 1996-443187/44.

P-PSDB; AAW04891.

XX

PT Neisseria meningitidis antigen, highly conserved between different  
 PT strains - useful for prodn. of antibodies for immunisation against, or  
 PT diagnosis of, N. meningitidis infection.

PS Claim 12; Fig 1; 117pp; English.

XX A proteinase K resistant surface protein has been isolated from 4 strains  
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,  
 CC antigenic fragments of antibodies can be used in a vaccine for the  
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in  
 CC humans. The antibodies may also be used diagnostically to detect N.  
 CC meningitidis infection. The antigen may also be used to detect antibodies  
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,  
 CC or their fragments, can be used as probes for the detection of pathogenic  
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 2; Length 830;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;  
 Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCATTGCGACACTGATTCCTCTCCGCGCGCGCGCACTGCGGAA 60  
 DB 143 ATGAAAAAGCATTGCGACACTGATTCCTCTCCGCGCGCGCGCACTGCGGAA 202  
 QY 61 GCGCATCCGCGCTTTAGCTCCAAAGCGATCCGACACGCAAAAGCTCAAGCTCTTTA 120  
 DB 203 GCGCATCCGCGCTTTAGCTCCAAAGCGATCCGACACGCAAAAGCTCAAGCTCTTTA 262  
 QY 121 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 180  
 DB 263 GGTTCGCAAGGCTTCAGCCCGGCTATCTCCGAGGCTACCGCATCAAGACCTCCGC 322  
 QY 181 TTGCGCGCTCGATTACACGCGCTACAAAACTATAAGCCCATCCACCGATTTCAACTT 240  
 DB 323 TTGCGCGCTCGATTACACGCGCTACAAAACTATAAGCCCATCCACCGATTTCAACTT 382  
 QY 241 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCACAAACCGTAT 300  
 DB 383 TACAGCATCGCGCTCGCCATTTCAGCTTCGACACCCCAATCGCCGTCACAAACCGTAT 442  
 QY 301 CTCGCGCGGCTTCAGCTTCACCGCGCTCAACCGCGCTTCGAGCTGGGCGGAGGACGCTTC 360  
 DB 443 CTCGCGCGGCTTCAGCTTCACCGCGCTCAACCGCGCTTCGAGCTGGGCGGAGGACGCTTC 502  
 QY 361 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 420  
 DB 503 AGCCAAACCTCATCGGCTCGCGCTATTGACGGCGCTAAGCTATGCCGTTACCCCGAAT 562  
 QY 421 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480  
 DB 563 GTCGATTTGGATGCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 622  
 QY 481 GTCGATTTGGGGAAGTGTCCGCTCGCGCTGCGCTCAAAATTCGA 525  
 DB 623 GTCGATTTGGGGAAGTGTCCGCTCGCGCTGCGCTCAAAATTCGA 667

RESULT 4

ACA64711  
 ID ACA64711 standard; DNA; 830 BP.

AC ACA64711;

XX 18-JUN-2003 (first entry)

DE N. meningitidis lipopolysaccharide gene.

XX Superantigen; ds; gene; SAG; staphylococcal enterotoxin; tumour; cancer;  
 KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;  
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;  
 KW tumouricidal immunocyte; antitumour.

XX OS Neisseria meningitidis.

XX PN US2002177551-A1.

XX PD 28-NOV-2002.

XX PF 30-MAY-2001; 2001US-00870759.

XX PR 31-MAY-2000; 2000US-0208128P.

XX PA (TERM/) TERMAN D S.

XX PI Terman DS;

XX DR WPI; 2003-361759/34.

XX DR P-PSDB; ABU79079.

XX PT A mammalian cell receptor, useful in the treatment of cancer by binding

XX PT to tumor associated lipids where the binding induces energy or apoptosis

XX PT in T cells and antigen presenting cells.

XX PS Disclosure; Page; 167pp; English.

XX CC The invention relates to a mammalian cell receptor, useful in the

XX CC treatment of cancer, which binds to tumor associated lipids and induces

XX CC energy or apoptosis in the T cells and antigen presenting cells (APCs).

XX CC Also included are a mammalian cell useful in the treatment of cancer

XX CC where the receptor which binds tumor associated lipids and induces

XX CC cellular inactivation or death is deleted or functionally deactivated,

XX CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal

XX CC (by allowing tumour associated lipids to contact immunocytes in which

XX CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,

XX CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,

XX CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or

XX CC deleted), a construct useful in the treatment of cancer comprising a

XX CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell

XX CC useful in the treatment of cancer (where an adaptor protein which

XX CC inhibits T cell activation by tumour associated antigens is deleted or

XX CC functionally deactivated), a composition useful in the treatment of

XX CC cancer (comprising a lipid raft conjugated to a superantigen), producing

XX CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by

XX CC allowing tumour associated lipids to contact immunocytes, in which

XX CC receptors for the lipids are inactivated or deleted to produce a

XX CC tumouricidal immunocyte population, and administering (M3) a tumouricidal APC

XX CC activated immunocytes to the host), producing (M3) a tumouricidal APC

XX CC population ex vivo in a mammal (by allowing a tumour associated lipid to

XX CC contact APCs, in which receptors for the tumour associated lipids are

XX CC inactivated or deleted to produce a tumouricidally activated population,

XX CC and administering APCs to the host), producing a tumouricidal T cell

XX CC population ex vivo in a mammal (by allowing a tumour associated lipids to

XX CC contact T cells, in which adaptor proteins, which inhibit T cell

XX CC activation by tumour associated antigens, are deleted or functionally

XX CC deactivated to produce a tumouricidal population of T cells, and

XX CC administering the tumouricidally activated T cells to the host, or

XX CC allowing a superantigen-lipid raft to contact T cells ex vivo, and

XX CC administering the tumouricidally activated T cells to the host), treating

XX CC (M5) cancer in a mammal (by administering a lipid binding molecule which

XX CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)

XX CC a tumouricidal T cell population in vivo in a mammal (by allowing a

XX CC tumour associated antigen to contact immunocytes in which adaptor

XX CC proteins which inhibit T cell activation by tumour associated antigens

XX CC are deleted or functionally deactivated) and producing (M7) a

XX CC tumouricidal T cell population ex vivo in a mammal comprising allowing a

XX CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The

XX CC receptors, methods and compositions are useful for treating cancers and

XX CC tumours. Bacterial superantigens are co-administered or administered as

XX CC fusion constructs with anti-tumour proteins or motifs. The present

XX CC sequence encodes an anti-tumour protein which is co-administered with or

XX CC incorporated into a fusion construct with a superantigen. Note: The

XX CC sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format from the US patent

XX CC office website at "seqdata.uspto.gov/sequence.html?docID=20020177551"

XX SQ Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 525; DB 8; Length 830;

XX Best Local Similarity 100.0%; Pred. No. 5.3e-125; Indels 0; Gaps 0;

XX Matches 525; Conservative 0; Mismatches 0;

QY 1 ATGAAAAAGCACTTGGCCACACTGATTGGCTTCCCGCGCGCGCGCACTGGCGGAA 60

DB 143 ATGAAAAAGCACTTGGCCACACTGATTGGCTTCCCGCGCGCGCGCACTGGCGGAA 202

QY 61 GCGGCATCCGGCTTTTACGTCCAAAGCGGATCCGACACGCAAAAGCCCTCAAGCTTTTA 120

DB 203 GCGGCATCCGGCTTTTACGTCCAAAGCGGATCCGACACGCAAAAGCCCTCAAGCTTTTA 262

QY 121 GGTTCCTGCAAGGGCTTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGCTCCGC 180

DB 263 GGTTCCTGCAAGGGCTTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGCTCCGC 322

QY 181 TTTCGCGCTCGATTACACGCGCTTACAAAACACTATAAGCCCGCATCCACCGATTTCAAACTT 240

DB 323 TTTCGCGCTCGATTACACGCGCTTACAAAACACTATAAGCCCGCATCCACCGATTTCAAACTT 382

QY 241 TCAGCATCCGGCTTCGCCATTTCAGCTTCGACACCCCAATCGCCCTCAAAACGGTAT 300

DB 383 TACAGCATCCGGCTTCGCCATTTCAGCTTCGACACCCCAATCGCCCTCAAAACGGTAT 442

QY 301 CTCGGCGCGCTTCAGGCTCAACCGCGCTCCGTCGCTGGCGGCGAGCAGCTTC 360

DB 443 CTCGGCGCGCTTCAGGCTCAACCGCGCTCCGTCGCTGGCGGCGAGCAGCTTC 502

QY 361 AGCCAAACCTCCATCCGCTCCGCGCTTATGACGGGCGTAAGCTATGCCGCTTACCCGGAAT 420

DB 503 AGCCAAACCTCCATCCGCTCCGCGCTTATGACGGGCGTAAGCTATGCCGCTTACCCGGAAT 562

QY 421 GTTCGATTGGATTCGGCGCTACCGCTTACAACTACATCGGCAAAAGTCAACTGTCAAAAAC 480

DB 563 GTTCGATTGGATTCGGCGCTACCGCTTACAACTACATCGGCAAAAGTCAACTGTCAAAAAC 622

QY 481 GTTCGATTGGCGGAAGTTCGCTCCGCGTCCGCGTCCGCGTCAAAATTCGA 525

DB 623 GTTCGATTGGCGGAAGTTCGCTCCGCGTCCGCGTCCGCGTCAAAATTCGA 667

RESULT 5

ADF4315

ID ADF4315 standard; DNA; 830 BP.

XX ADF4315;

XX ADF4315;

DT 12-FEB-2004 (first entry)

XX N. meningitidis lipopolysaccharide DNA seq id 35.

XX receptor; lipid-based tumour associated antigen; cytostatic;

XX antimicrobial; gene therapy; neoplastic disease; tumour; cancer;

XX infectious disease; lipopolysaccharide; LPS; ds.

XX Neisseria meningitidis.

XX US2003157113-A1.

XX 21-AUG-2003.

XX 28-DEC-2000; 2000US-00751708.

XX 28-DEC-1999; 99US-0173371P.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2003-787326/74.

DR P-PSDB; ADF43316.

XX New receptor in a mammalian cell that inhibits regular activation by  
PT receptors specific for lipid-based tumor associated antigens, useful for  
PT treating a neoplastic disease or tumor, and infectious diseases.

XX Disclosure; SEQ ID NO 35; 151pp; English.

XX The invention describes a receptor in a mammalian cell that inhibits  
CC regular activation by receptors specific for lipid-based tumour  
CC associated antigen. The receptor has cytostatic and antimicrobial  
CC properties and is suitable for use in gene therapy. The receptors,  
CC methods and compositions are useful for treating a neoplastic disease or  
CC tumour (cancer), and infectious diseases. This sequence encodes Neisseria  
CC meningitidis lipopolysaccharide (LPS) to which tumour cells develop  
CC immunity.

XX Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;

Query Match 100.0%; Score 525; DB 10; Length 830;

Best Local Similarity 100.0%; Pred. No. 5.3e-125;

Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAAAAGCACTTGCACACTGATTGCTTCCCTCGCTCTCCGGCGCGCACTGGCGGAA	60
Db	143	ATGAAAAAGCACTTGCACACTGATTGCTTCCCTCGCTCTCCGGCGCGCACTGGCGGAA	202
Qy	61	GGCGCATCCGGCTTTACGTCGAAGCCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA	120
Db	203	GGCGCATCCGGCTTTACGTCGAAGCCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA	262
Qy	121	GGTTCGCAAAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	180
Db	263	GGTTCGCAAAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	322
Qy	181	TTGCGCGTCGATTACACGGCTACAAAACATAAAGCCGATCAACGATTTCAAACTT	240
Db	323	TTGCGCGTCGATTACACGGCTACAAAACATAAAGCCGATCAACGATTTCAAACTT	382
Qy	241	TACAGCATCGCGCGCTTCAGCTTACGATTCGACACCCCAATCGCCGCTCAAAACCGTAT	300
Db	383	TACAGCATCGCGCGCTTCAGCTTACGATTCGACACCCCAATCGCCGCTCAAAACCGTAT	442
Qy	301	CTCGCGCGCGCTTCAGCTTCAACCGCGCTCCGCTCGACTTGGGCGGCGAGCAGCTTC	360
Db	443	CTCGCGCGCGCTTCAGCTTCAACCGCGCTCCGCTCGACTTGGGCGGCGAGCAGCTTC	502
Qy	361	AGCCAAACCTCATCGGCTTCGGCGTATTGACGGCGGTAAAGCTATGCCGTTACCCCGAAT	420
Db	503	AGCCAAACCTCATCGGCTTCGGCGTATTGACGGCGGTAAAGCTATGCCGTTACCCCGAAT	562
Qy	421	GTCGATTTGGATGCGGCTACCGCTACCACTACGCAAGTCAACACTGTCAAAAC	480
Db	563	GTCGATTTGGATGCGGCTACCGCTACCACTACGCAAGTCAACACTGTCAAAAC	622
Qy	481	GTCGATTTGGATGCGGCTACCGCTACCGCTCGCGCTCAAAATCTGA	525
Db	623	GTCGATTTGGATGCGGCTACCGCTCGCGCTCAAAATCTGA	667

# RESULT 6

Continuation (15 of 15) of AAA81490 from base 1400001 (N. meningitidis B full length gen

WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490

Fragment Name Begin End

WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000

WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668

Query Match 99.4%; Score 521.8; DB 3; Length 37668;

Best Local Similarity 99.6%; Pred. No. 8.4e-124;

Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ATGAAAAAGCACTTGCACACTGATTGCTTCCCTCGCTCTCCGGCGCGCACTGGCGGAA	60
Db	20578	ATGAAAAAGCACTTGCACACTGATTGCTTCCCTCGCTCTCCGGCGCGCACTGGCGGAA	20519
Qy	61	GGCGCATCCGGCTTTACGTCGAAGCCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA	120
Db	20518	GGCGCATCCGGCTTTACGTCGAAGCCGATGCGGCACACGCAAAAGCTTCAAGCTCTTTA	20459
Qy	121	GGTTCGCAAAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	180
Db	20458	GGTTCGCAAAAGGCTTCAGCGCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC	20399
Qy	181	TTGCGCGTCGATTACACGGCTACAAAACATAAAGCCGATCAACGATTTCAAACTT	240
Db	20398	TTGCGCGTCGATTACACGGCTACAAAACATAAAGCCGATCAACGATTTCAAACTT	20339
Qy	241	TACAGCATCGCGCGCTTCAGCTTACGATTCGACACCCCAATCGCCGCTCAAAACCGTAT	300
Db	20338	TACAGCATCGCGCGCTTCAGCTTACGATTCGACACCCCAATCGCCGCTCAAAACCGTAT	20279
Qy	301	CTCGCGCGCGCTTCAGCTTCAACCGCGCTCCGCTCGACTTGGGCGGCGAGCAGCTTC	360
Db	20278	CTCGCGCGCGCTTCAGCTTCAACCGCGCTCCGCTCGACTTGGGCGGCGAGCAGCTTC	20219
Qy	361	AGCCAAACCTCATCGGCTTCGGCGTATTGACGGCGGTAAAGCTATGCCGTTACCCCGAAT	420
Db	20218	AGCCAAACCTCATCGGCTTCGGCGTATTGACGGCGGTAAAGCTATGCCGTTACCCCGAAT	20159
Qy	421	GTCGATTTGGATGCGGCTACCGCTACCACTACGCAAGTCAACACTGTCAAAAC	480
Db	20158	GTCGATTTGGATGCGGCTACCGCTACCACTACGCAAGTCAACACTGTCAAAAC	20099
Qy	481	GTCGATTTGGATGCGGCTACCGCTACCGCTCGCGCTCAAAATCTGA	525
Db	20098	GTCGATTTGGATGCGGCTACCGCTCGCGCTCAAAATCTGA	20054

# RESULT 7

Continuation (7 of 15) of AAA81490 from base 600001 (N. meningitidis B full length genome

WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490

Fragment Name Begin End

WP	AAA81490_00	1	110000
WP	AAA81490_01	100001	210000
WP	AAA81490_02	200001	310000
WP	AAA81490_03	300001	410000
WP	AAA81490_04	400001	510000
WP	AAA81490_05	500001	610000
WP	AAA81490_06	600001	710000
WP	AAA81490_07	700001	810000
WP	AAA81490_08	800001	910000
WP	AAA81490_09	900001	1010000
WP	AAA81490_10	1000001	1110000
WP	AAA81490_11	1100001	1210000
WP	AAA81490_12	1200001	1310000
WP	AAA81490_13	1300001	1410000
WP	AAA81490_14	1400001	1437668

Query Match 99.4%; Score 521.8; DB 3; Length 110000;

Best Local Similarity 99.6%; Pred. No. 1.1e-123;

Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCCGCCGCACTGGCGGAA	60
Db	90785	ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCCGCCGCACTGGCGGAA	90726
QY	61	GGCGCATCCGGCTTTTACGTCCAAAGCCGATGCGCACAAGCAAAAGCCCTCAAGCTCTTTA	120
Db	90725	GGCGCATCCGGCTTTTACGTCCAAAGCCGATGCGCACAAGCAAAAGCCCTCAAGCTCTTTA	90666
QY	121	GGTTCTGCAAAAGGCTTACGCCCGCCGCACTCCGCAAGGCTACCGCATCAACGACCTCCGC	180
Db	90665	GGTTCTGCAAAAGGCTTACGCCCGCCGCACTCCGCAAGGCTACCGCATCAACGACCTCCGC	90606
QY	181	TTCCGCGTCCGATTACACGGCGCTCAAAAACTATAAAGCCCGCATCCACCGATTTCAAACTT	240
Db	90605	TTCCGCGTCCGATTACACGGCGCTCAAAAACTATAAAGCCCGCATCCACCGATTTCAAACTT	90546
QY	241	TACAGATCGCGCGCTCCGCACTTACGATTCGACACCCCAATCGCCCGTCAAAACGATAT	300
Db	90545	TACAGATCGCGCGCTCCGCACTTACGATTCGACACCCCAATCGCCCGTCAAAACGATAT	90486
QY	301	CTCGCGCGCGCTTACGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGCGACAGCTTC	360
Db	90485	CTCGCGCGCGCTTACGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGCGACAGCTTC	90426
QY	361	AGCCAAACCTCCATCGCGCTTCGCGGTATTTGACGGCGGTAAGCTATGCGGTTACCCCGAAT	420
Db	90425	AGCCAAACCTCCATCGCGCTTCGCGGTATTTGACGGCGGTAAGCTATGCGGTTACCCCGAAT	90366
QY	421	GTCGATTGGATGCGCGGTACCGCTTACCACTACATCGGCAAAAGTCAACACTGTCAAAAAC	480
Db	90365	GTCGATTGGATGCGCGGTACCGCTTACCACTACATCGGCAAAAGTCAACACTGTCAAAAAC	90305
QY	481	GTCCGTTCCGGCGAACTGTCCGCTCGCGCTCAAAATTCGA	525
Db	90305	GTCCGTTCCGGCGAACTGTCCGCTCGCGCTCAAAATTCGA	90261
RESULT 8			
AAAF21608/c			
ID	AAAF21608 standard; DNA; 349980 BP.		
XX			
AC	AAAF21608;		
XX			
DT	13-MAR-2001 (first entry)		
XX	Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.		
DE			
XX			
KW	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;		
KW	diagnosis; antigen; detection; infection; gene therapy; antibacterial;		
ds.			
XX			
OS	Neisseria meningitidis.		
XX			
PN	WO200066791-A1.		
XX			
PD	09-NOV-2000.		
XX			
PF	08-MAR-2000; 2000WO-US0005928.		
XX			
PR	30-APR-1999; 99US-0132068P.		
PR	08-OCT-1999; 99WO-US023573.		
PR	28-FEB-2000; 2000GB-00004695.		
XX			
XX	(CHIR ) CHIRON CORP.		
PA	(GENO-) INST GENOMIC RES.		
XX			
PI	Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;		
PI	Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M,		
PI	Rappuoli R, Frazer CM, Grandi G;		
XX			
DR	WPI; 2000-647603/62.		
XX			

Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections.

Claim 7; Appendix A; 692pp; English.

The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used

Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 U; 0 Other;

Query Match 99.4%; Score 521.8; DB 3; Length 349980;  
Best Local Similarity 99.6%; Pred. No. 1.4e-123;  
Matches 523; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCCGCCGCACTGGCGGAA 60  
Db 90786 ATGAAAAAGCACTTCCACACATGATTGCCCTCGCTCTCCGCGCCCGCCGCACTGGCGGAA 90727

QY 61 GGCGCATCCGGCTTTTACGTCCAAAGCCGATGCGCACAAGCAAAAGCCCTCAAGCTCTTTA 120  
Db 90726 GGCGCATCCGGCTTTTACGTCCAAAGCCGATGCGCACAAGCAAAAGCCCTCAAGCTCTTTA 90667

QY 121 GGTTCGCAAAAGGCTTACGCCCGCCGCACTCCGCAAGGCTACCGCATCAACGACCTCCGC 180  
Db 90666 GGTTCGCAAAAGGCTTACGCCCGCCGCACTCCGCAAGGCTACCGCATCAACGACCTCCGC 90607

QY 181 TTCGCGCTCGATTACACGGCGCTACAAAACTATAAAGCCCGCATCCACCGATTTCAAACTT 240  
Db 90606 TTCGCGCTCGATTACACGGCGCTACAAAACTATAAAGCCCGCATCCACCGATTTCAAACTT 90547

QY 241 TACAGATCGCGCGCTCCGCACTTACGATTCGACACCCCAATCGCCCGTCAAAACGATAT 300  
Db 90546 TACAGATCGCGCGCTCCGCACTTACGATTCGACACCCCAATCGCCCGTCAAAACGATAT 90487

QY 301 CTCGGCGCGCTTACGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGCGACAGCTTC 360  
Db 90486 CTCGGCGCGCTTACGCTCAACCGCGCTCCGTCGACTTGGCGGCGAGCGACAGCTTC 90427

QY 361 AGCCAAACCTCCATCGCGCTTCGCGGTATTTGACGGCGGTAAGCTATGCGGTTACCCCGAAT 420  
Db 90426 AGCCAAACCTCCATCGCGCTTCGCGGTATTTGACGGCGGTAAGCTATGCGGTTACCCCGAAT 90367

QY 421 GTCGATTGGATGCGCGGTACCGCTTACCACTACATCGGCAAAAGTCAACACTGTCAAAAAC 480  
Db 90366 GTCGATTGGATGCGCGGTACCGCTTACCACTACATCGGCAAAAGTCAACACTGTCAAAAAC 90307

QY 481 GTCCGTTCCGGCGAACTGTCCGCTCGCGCTCAAAATTCGA 525  
Db 90306 GTCCGTTCCGGCGAACTGTCCGCTCGCGCTCAAAATTCGA 90262

RESULT 9  
AAAF21608/c  
ID AAF21608 standard; DNA; 850 BP.

XX AC AAT39041;  
 XX 16-OCT-2003 (revised)  
 XX 22-DEC-1996 (first entry)  
 XX  
 XX Proteinase K resistant N. meningitidis 22 kD surface protein.  
 XX  
 XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
 KW antibody; detection; probe; surface protein; ss.  
 XX  
 XX Neisseria meningitidis; strain Z4063.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 208..732 /\*tag= a  
 FT sig\_peptide 208..264 /\*tag= b  
 FT mat\_peptide 265..729 /\*tag= c  
 FT  
 XX W09629412-A1.  
 XX  
 XX 26-SEP-1996.  
 XX  
 XX 15-MAR-1996; 96WO-CA000157.  
 XX  
 XX 17-MAR-1995; 95US-00406362.  
 PR 04-AUG-1995; 95US-0001983P.  
 XX  
 XX (IAFB-) IAF BIO VAC INC.  
 XX  
 XX Brodeur BR, Martin D, Hamel J, Rioux C;  
 XX  
 XX WPI; 1996-443187/44.  
 DR P-PSDB; AAW04893.  
 DR  
 XX Neisseria meningitidis antigen, highly conserved between different  
 PT strains - useful for prodn. of antibodies for immunisation against, or  
 PT diagnosis of, N. meningitidis infection.  
 PT  
 XX Claim 12; Fig 9; 117pp; English.  
 PS  
 XX A proteinase K resistant surface protein has been isolated from 4 strains  
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,  
 CC antigenic fragments of antibodies can be used in a vaccine for the  
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in  
 CC humans. The antibodies may also be used diagnostically to detect N.  
 CC meningitidis infection. The antigen may also be used to detect antibodies  
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,  
 CC or their fragments, can be used as probes for the detection of pathogenic  
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 850 BP; 208 A; 273 C; 185 G; 184 T; 0 U; 0 Other;  
 SQ  
 Query Match 98.8%; Score 518.6; DB 2; Length 850;  
 Best Local Similarity 99.2%; Pred. NO. 2.3e-123;  
 Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ATGAAGAAAGCACTGCGACACTGATTCCTCGCTCTCCGCGCGCGCGCGCGGAA 60  
 DB 208 ATGAAGAAAGCACTGCGACACTGATTCCTCGCTCTCCGCGCGCGCGCGCGGAA 267  
 QY 61 GGCGCATCCGGCTTTTACGTCGAAGCCGATGCGGACACGCAAAAGCTCAAGCTCTTTA 120  
 DB 268 GGCGCATCCGGCTTTTACGTCGAAGCCGATGCGGACACGCAAAAGCTCAAGCTCTTTA 327  
 QY 121 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 180  
 DB 328 GGTTCGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGCACTCCGC 387  
 QY 181 TTCGCGTCGATTACACGGCTACAAAACCTATAAGCCCATCCACCGATTCAACTT 240

DB 388 TTCGCCGTCGATTACACGCGCTACAAAACCTATATAAGCCCATCCACGGATTTCAAACCTT 447  
 QY 241 TACAGCATCGCGCGCTCCGCCATTTACGACTTCGACACACCCCAATCGCCGTCACACCGTAT 300  
 DB 448 TACAGCATCGCGCGCTCCGCCATTTACGACTTCGACACACCCCAATCGCCGTCACACCGTAT 507  
 QY 301 CTGCGCGCGCTTGAGCTCAACCGGCTCCCTCGACTTGGGGGCGGAGGACAGCTTC 360  
 DB 508 CTGCGCGCGCTTGAGCTCAACCGGCTCCCTCGACTTGGGGGCGGAGGACAGCTTC 567  
 QY 361 AGCCAAACCTCCATCGCGCTGATTTGACGGGCTTAAGCTATGCCGTTACCCCGAAT 420  
 DB 568 AGCCAAACCTCCATCGCGCTGATTTGACGGGCTTAAGCTATGCCGTTACCCCGAAT 627  
 QY 421 GTCGATTTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480  
 DB 628 GTCGATTTGGATCGCGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 687  
 QY 481 GTCGTTCCGGCGAAGTGTCCGTCGGCGTGGCGGCTCAAAATTCGA 525  
 DB 688 GTCGTTCCGGCGAAGTGTCCGTCGGCGTGGCGGCTCAAAATTCGA 732  
 RESULT 10  
 ABS67381  
 ID ABS67381 standard; DNA; 710 BP.  
 XX  
 AC ABS67381;  
 XX  
 XX 29-NOV-2002 (first entry)  
 XX  
 DE Neisseria gonorrhoeae outer membrane gene #1.  
 XX  
 KW Gram-negative bacterial bleb; PorB; outer membrane protein;  
 KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;  
 KW protective antigen; antibacterial; vaccine; gene; ds.  
 XX  
 OS Neisseria gonorrhoeae.  
 XX  
 XX WO200262380-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 08-FEB-2002; 2002WO-EP001356.  
 XX  
 PR 08-FEB-2001; 2001GB-00003169.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;  
 XX WPI; 2002-657510/70.  
 DR P-PSDB; ABG91063.  
 XX  
 XX Novel gram-negative bacterial bleb presenting on its surface PorB outer  
 PT membrane protein from Chlamydia trachomatis or protective antigen from  
 PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.  
 XX  
 PS Disclosure; Page 54; 75pp; English.  
 XX  
 CC The present invention relates to a new gram-negative bacterial bleb  
 CC presenting on its surface the PorB outer membrane protein from Chlamydia  
 CC trachomatis, or a protective antigen from C. pneumoniae. The invention is  
 CC useful for preventing C. trachomatis or C. pneumoniae infection in a  
 CC host. The present nucleic acid sequence represents a Neisseria  
 CC gonorrhoeae gene as described in the invention  
 XX  
 SQ Sequence 710 BP; 171 A; 228 C; 160 G; 151 T; 0 U; 0 Other;  
 Query Match 95.7%; Score 502.6; DB 6; Length 710;  
 Best Local Similarity 97.3%; Pred. No. 2.9e-119;  
 Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTGCACACTGATGGCCCTCGCTCTCCCGCGCGCGCACTGGCGGAA 60  
 DB 141 ATGAAAAAGCACTTGCACACTGATGGCCCTCGCTCTCCCGCGCGCGCACTGGCGGAA 200  
 QY 61 GCGCATCGGCTTTTACGTCAAGCCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 120  
 DB 201 GCGCATCGGCTTTTACGTCAAGCCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 260  
 QY 121 GGTTCGCAAGGCTTCAGCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180  
 DB 261 GGTTCGCAAGGCTTCAGCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 320  
 QY 181 TTCCGCGTTCGATACACGCGCTTCAAAAACTATAAGCCCTTCCACCGATTTCAAACCTT 240  
 DB 321 TTCCGCGTTCGATACACGCGCTTCAAAAACTATAAGCCCTTCCACCGATTTCAAACCTT 380  
 QY 241 TACAGATCGGCGGCTTCGCGCTTTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTAT 300  
 DB 381 TACAGATCGGCGGCTTCGCGCTTTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTAT 440  
 QY 301 CTCGCGCGGCTTCGAGCCTCAACGCGCTCCGTCGACTTCGGCGGCGAGCGACAGCTTC 360  
 DB 441 TTCGCGCGGCTTCGAGCCTCAACGCGCTTCGCGGCTTCGGCGGCGAGCGACAGCTTC 500  
 QY 361 AGCCAAACCTCCATCGGCGCTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 420  
 DB 501 AGCCAAACCTCCGCGGCTTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 560  
 QY 421 GTCGATTCGCGGCTTCGCGCTTACGCTACAACTACATCGGCAAAAGTCAAGCTGTCAAAC 480  
 DB 561 GTCGATTCGCGGCTTCGCGCTTACGCTACAACTACATCGGCAAAAGTCAAGCTGTCAAAC 620  
 QY 481 GTCGCTTCGCGCAACTGTCGCGTTCGCGGCTCAAAATTCGA 525  
 DB 621 GTCGCTTCGCGCAACTGTCGCGGCTCAAAATTCGA 665

RESULT 11

AAT39042  
 ID AAT39042 standard; DNA; 810 BP.  
 XX AC AAT39042;  
 XX DT 16-OCT-2003 (revised)  
 XX DT 22-DEC-1996 (first entry)  
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.  
 XX Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;  
 KW antibody; detection; probe; surface protein; ss.  
 XX OS Neisseria meningitidis; strain b2.

Key	Location/Qualifiers
FT CDS	241..765
FT FT	/*tag= a
FT sig_peptide	241..297
FT FT	/*tag= b
FT sig_peptide	298..762
FT FT	/*tag= c

XX WO9629412-A1.  
 XX PD 26-SEP-1996.  
 XX PF 15-MAR-1996; 96WO-CA000157.  
 XX PR 17-MAR-1995; 95US-00406362.  
 XX PR 04-AUG-1995; 95US-0001983F.  
 XX PA (IAFB-) IAF BIO VAC INC.  
 XX PI Brodeur BR, Martin D, Hamel J, Rioux C;

XX WPI; 1996-443187/44.  
 DR P-PSDB; AAW04894.  
 XX Neisseria meningitidis antigen, highly conserved between different  
 PT strains - useful for prodn. of antibodies for immunisation against, or  
 PT diagnosis of, N. meningitidis infection.  
 XX Claim 12; Fig 10; 117pp; English.  
 PS A proteinase K resistant surface protein has been isolated from 4 strains  
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,  
 CC antigenic fragments of antibodies can be used in a vaccine for the  
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in  
 CC humans. The antibodies may also be used diagnostically to detect N.  
 CC meningitidis infection. The antigen may also be used to detect antibodies  
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,  
 CC or their fragments, can be used as probes for the detection of pathogenic  
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)  
 XX Sequence 810 BP; 186 A; 260 C; 186 G; 178 T; 0 U; 0 Other;

Query Match 95.7%; Score 502.6; DB 2; Length 810;  
 Best Local Similarity 97.3%; Pred. No. 36-119;  
 Matches 511; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 ATGAAAAAGCACTTGCACACTGATGGCCCTCGCTCTCCCGCGCGCGCACTGGCGGAA 60  
 DB 241 ATGAAAAAGCACTTGCACACTGATGGCCCTCGCTCTCCCGCGCGCGCACTGGCGGAA 300  
 QY 61 GCGCATCGGCTTTTACGTCAAGCCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 120  
 DB 301 GCGCATCGGCTTTTACGTCAAGCCGATGCGCACAGCAAAAGCTTCAAGCTCTTTA 360  
 QY 121 GGTTCGCAAGGCTTCAGCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180  
 DB 361 GGTTCGCAAGGCTTCAGCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 420  
 QY 181 TTCGCGCTCGATTCACGCGCTTACAAAACTATAAGCCCTTCCACCGATTTCAAACCTT 240  
 DB 421 TTCGCGCTCGATTCACGCGCTTACAAAACTATAAGCCCTTCCACCGATTTCAAACCTT 480  
 QY 241 TACAGATCGGCGGCTTCGCGCTTTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTAT 300  
 DB 481 TACAGATCGGCGGCTTCGCGCTTTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTAT 540  
 QY 301 CTCGCGCGGCTTCGAGCCTCAACGCGCTCCGTCGACTTCGGCGGCGAGCGACAGCTTC 360  
 DB 541 TTCGCGCGGCTTCGAGCCTCAACGCGCTTCGCGGCTTCGGCGGCGAGCGACAGCTTC 600  
 QY 361 AGCCAAACCTCCATCGGCGCTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 420  
 DB 601 AGCCAAACCTCCGCGGCTTCGCGCTTATGACGGGCTAAGCTATGCGGTTACCCCGAAT 660  
 QY 421 GTCGATTCGCGCAACTGTCGCGTTCGCGGCTCAAAATTCGA 525  
 DB 721 GTCGCTTCGCGCAACTGTCGCGGCTCAAAATTCGA 765

RESULT 12

AAT39040  
 ID AAT39040 standard; DNA; 710 BP.  
 XX AC AAT39040;  
 XX DT 16-OCT-2003 (revised)  
 XX DT 22-DEC-1996 (first entry)  
 XX DE Proteinase K resistant N. meningitidis 22 kD surface protein.

```

XX KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
XX antibody; detection; probe; surface protein; ss.
XX OS Neisseria meningitidis; strain MCH88.
XX FH Key Location/Qualifiers
XX CDS 116..643
XX FT /*tag= a
XX sig_peptide 116..172
XX FT /*tag= b
XX mat_peptide 173..640
XX FT /*tag= c
XX PN W09629412-A1.
XX PD 26-SEP-1996.
XX PF 15-MAR-1996; 96WO-CA000157.
XX PR 17-MAR-1995; 95US-00406362.
XX PR 04-AUG-1995; 95US-0001983P.
XX PA (IAPB-) IAP BIO VAC INC.
XX PI Brodeur BR, Martin D, Hamel J, Rioux C;
XX WPI; 1996-443187/44.
XX DR P-PSDB; AAW04892.
XX OS Neisseria meningitidis antigen, highly conserved between different
XX strains - useful for prodn. of antibodies for immunisation against, or
XX diagnosis of, N. meningitidis infection.
XX PS Claim 12; Fig 8; 117pp; English.
XX CC A proteinase K resistant surface protein has been isolated from 4 strains
XX of N. meningitidis (AAR39039 to AAT39042). The isolated 22 kD antigen,
XX antigenic fragments of antibodies can be used in a vaccine for the
XX prevention of infection by N. meningitidis or by N. gonorrhoeae in
XX humans. The antibodies may also be used diagnostically to detect N.
XX meningitidis infection. The antigen may also be used to detect antibodies
XX specific to N. meningitidis antigen. DNA sequences encoding the antigen,
XX or their fragments, can be used as probes for the detection of pathogenic
XX Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX SQ Sequence 710 BP; 174 A; 232 C; 148 G; 156 T; 0 U; 0 Other;

Query Match 93.6%; Score 491.2; DB 2; Length 710;
Best Local Similarity 97.0%; Pred. No. 2.5e-116;
Matches 512; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

QY 1 ATGAAAAGCACTTGCACACTGATTCGCTCCGCTCCGCGCGCGCACTGCGGAA 60
DB 116 ATGAAAAGCACTTGCACACTGATTCGCTCCGCTCCGCGCGCGCACTGCGGAA 175
QY 61 GCGCATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAGAACTCAAGCTCTTTA 120
DB 176 GCGCATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAGAACTCAAGCTCTTTA 235
QY 121 GGTTCGCAAGGTTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 180
DB 236 GGTTCGCAAGGTTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 295
QY 181 TTCGCGGTGATTACACGGCTTACAAAACATA---AAGCCCATCCACGATTTCAA 237
DB 296 TTCGCGGTGATTACACGGCTTACAAAACATA---AAGCCCATCCACGATTTCAA 355
QY 238 CTTTACAGCATCGCGCGTTCGCCATTTACGACTTCGACACCAATCGCCGTTCAACCG 297
DB 356 CTTTACAGCATCGCGCGTTCGCCATTTACGACTTCGACACCAATCGCCGTTCAACCG 415
QY 298 TATCTCGCGCGCTTGAGCCTCAACCGCGCTCCGCTCGACTTGCGGCGCAGCAGCAGC 357

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DB 416 TATCTCGCGCGCTTGAGCCTCAACCGCGCTCCGCTCGACTTTAACGGCAGCAGC 475
QY 358 TTACGCCAAACCTCCATCGGCTTATTGACGGCGGTAAGCTATGCGGTTACCCCG 417
DB 476 TTACGCCAAACCTCCATCGGCTTATTGACGGCGGTAAGCTATGCGGTTACCCCG 535
QY 418 AATGTCGATTTGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAA 477
DB 536 AATGTCGATTTGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAA 595
QY 478 AACGTCGTTCCGGCAACTGTCCGTCGGCGTGGCGTCAAAATCTGA 525
DB 596 AATGTCGTTCCGGCAACTGTCCGTCGGCGTGGCGTCAAAATCTGA 643

RESULT 13
ABZ38961
ID ABZ38961 standard; DNA; 525 BP.
XX AC ABZ38961;
XX DT 07-MAR-2003 (first entry)
XX DE N. gonorrhoeae nucleotide sequence SEQ ID 2511.
XX KW Antibacterial; infection; vaccine; gene therapy; gene; ds.
XX OS Neisseria gonorrhoeae.
XX FN W0200279243-A2.
XX PD 10-OCT-2002.
XX PF 12-FEB-2002; 2002WO-1B002069.
XX PR 12-FEB-2001; 2001GB-00003424.
XX PA (CHIR-) CHIRON SPA.
XX PI Fontana MR, Pizza M, Massignani V, Monaci E;
XX WPI; 2003-058415/05.
XX DR P-PSDB; ABP77991.
XX PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX medicament for treating or preventing N. gonorrhoeae infection.
XX PS Disclosure; Page 371; 815pp; English.
XX CC The present invention relates to proteins from Neisseria gonorrhoeae.
XX Also disclosed are the nucleic acid molecules encoding the proteins and
XX antibodies that specifically bind to the proteins. The composition
XX comprising the protein, nucleic acid or antibody is useful for the
XX manufacture of a medicament for treating or preventing N. gonorrhoeae
XX infection, this may be in the form of a vaccine or gene therapy.
XX Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
XX molecules of the invention
XX SQ Sequence 525 BP; 117 A; 188 C; 120 G; 100 T; 0 U; 0 Other;

Query Match 91.5%; Score 480.2; DB 10; Length 525;
Best Local Similarity 96.0%; Pred. No. 1.5e-113;
Matches 504; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 ATGAAAAGCACTTGCACACTGATTCGCTCCGCGCGCGCACTGCGGAA 60
DB 1 ATGAAAAGCACTTGCACACTGATTCGCTCCGCGCGCGCACTGCGGAA 60
QY 61 GCGCATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAGAACTCAAGCTCTTTA 120
DB 61 GCGCATCCGGCTTTTACGTCAAGCCGATGCGGCACACGCAAGAACTCAAGCTCTTTA 120

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QY 121 GGTTCTGCCAAGGCTTACAGCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180  
 Db 121 GGTTCTGCCAAGGCTTACAGCCGCGCATCTCCGAGGCTACCGCATCAACGACCTCCGC 180  
 QY 181 TTCGCGTGCATACACGCGCTACAAAACACTATA---AAGCCCAATCCACCGATTCAAA 237  
 Db 181 TTCGCGTGCATACACGCGCTACAAAACACTATA---AAGCCCAATCCACCGATTCAAA 240  
 QY 238 CTTTACAGCATCGCGCGCTCCGCGCATTTTACGACTTCGACACCCCAATTCGCCCGTCAAAACCG 297  
 Db 241 CTTTACAGCATCGCGCGCTCCGCGCATTTTACGACTTCGACACCCCAATTCGCCCGTCAAAACCG 300  
 QY 298 TATCTCGCGCGCGCTTGAAGCTCAACCGCGCTTCGTCGACTTGGCGGCGAGCGACAGC 357  
 Db 301 TATCTCGCGCGCGCTTGAAGCTCAACCGCGCTTCGTCGACTTGGCGGCGAGCGACAGC 360  
 QY 358 TTCAGCAAACTCCATCGCGCTCCGCGCTATTCGAGCGGCTAAGCTATGCGCTTACCCCG 417  
 Db 361 TTCAGCAAACTCCGCGCGCTCCGCGCTATTCGAGCGGCTAAGCTATGCGCTTACCCCG 420  
 QY 418 AATGTCGATTTGGATCGCGCTACCGCTCAACACTACATCGGCAAAAGTCAACACTGTCAAA 477  
 Db 421 AATGTCGATTTGGATCGCGCTACCGCTCAACACTACATCGGCAAAAGTCAACACTGTCAAA 480  
 QY 478 AAGTCCTGTCGCGCAATGTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCT 522  
 Db 481 AAGTCCTGTCGCGCAATGTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCTCGCGCT 525

## RESULT 14

ADL13425  
 ID ADL13425 standard; DNA; 468 BP.  
 AC ADL13425;  
 DT 03-JUN-2004 (first entry)  
 XX Neisseria meningitidis H44/76 mature NspA-encoding DNA.

XX Neisserial surface protein A; NspA; refolding; recombinant production;  
 KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;  
 KW invasive bacterial disease; bacteraemia; meningitis;  
 KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;  
 KW antibacterial; gene therapy; gene; ds.  
 OS Neisseria meningitidis; H44/76.

Key Location/Qualifiers  
 CDS 1..468  
 /tag= b  
 /partial  
 /product= "Mature NspA"  
 /note= "No start codon given"  
 mat\_peptide 1..465  
 /tag= a  
 /product= "Mature NspA"

W02004020452-A2.

11-MAR-2004.

28-AUG-2003; 2003WO-EP010085.

30-AUG-2002; 2002GB-00020197.

(GLAXO) GLAXOSMITHKLINE BIOLOGICALS SA.  
 (UYUT-) RIJKSUNIV UTRECHT.

XX Biemanns R, Bos M, Denoel P, Feron C, Goraj K, Poolman J;  
 PI Tommassen J, Weynants V;  
 DR WPI: 2004-239150/22.  
 DR P-PSDB; ADL13426.

XX New refolded NspA protein, useful for preparing a composition for  
 PT diagnosing, treating or preventing infection caused by Neisseria  
 PT meningitidis or Neisseria gonorrhoeae.  
 XX Example 1; Fig 2; 62pp; English.  
 XX The invention relates to an isolated refolded Neisserial surface protein  
 CC A (NspA) from Neisseria meningitidis or Neisseria gonorrhoeae. The  
 CC invention also relates to the method of refolding an NspA protein; an  
 CC alkaline refolding buffer comprising ethanolamine and SB-12 (3-  
 CC dimethyldecylammonioethanesulphonate) for refolding an NspA protein; a  
 CC pharmaceutical composition comprising the refolded NspA protein, a  
 CC carrier and optionally one or more other Neisserial antigens; a method of  
 CC preventing or treating a Neisserial infection; an antibody immunospecific  
 CC for the NspA protein; and diagnosing a Neisserial infection. NspA has  
 CC characteristics which indicate that it is a potential vaccine candidate  
 CC for the development of subunit vaccines for the treatment of infections  
 CC caused by Neisseria meningitidis (meningococcus), which causes invasive  
 CC bacterial diseases such as bacteraemia and meningitis, or Neisseria  
 CC gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced  
 CC NspA could therefore be used to produce vaccine compositions and it could  
 CC also be used in the development of new antimicrobial agents, diagnostic  
 CC tests and in drug screening. However, recombinantly produced proteins are  
 CC frequently unable to adopt their biologically active conformations, and  
 CC yields may be very low due to mis-folding and aggregation of the protein.  
 CC The method of the invention provides an improved method for refolding the  
 CC NspA protein, and it is possible to increase the recovery of active  
 CC protein form partly purified inclusion bodies in amounts up to 100%  
 CC without the need for further purification. The refolded NspA protein is  
 CC useful for preparing a composition for diagnosing, treating or preventing  
 CC infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The  
 CC present sequence represents DNA encoding the mature NspA protein from  
 CC Neisseria meningitidis H44/76 which was amplified and cloned in an  
 CC example of the invention.

Sequence 468 BP; 105 A; 164 C; 106 G; 93 T; 0 U; 0 Other;

Query Match 88.5%; Score 464.8; DB 12; Length 468;  
 Best Local Similarity 99.6%; Pred. No. 1.4e-109;  
 Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 118 TTAGGTTCTGCCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAACGACCTC 177  
 Db 61 TTAGGTTCTGCCAAGGCTTCAGCCCGCATCTCCGAGGCTACCGCATCAACGACCTC 120  
 QY 178 CGCTTCGCGCTCGATTACACGCGCTACAAAACATAAAGCCCGCATCCACCGATTTCAAA 237  
 Db 121 CGCTTCGCGCTCGATTACACGCGCTACAAAACATAAAGCCCGCATCCACCGATTTCAAA 180  
 QY 238 CTTTACAGCATCGCGCGCTCGCGCATTTTACGACTTCGACACCCCAATTCGCCCGTCAACCG 297  
 Db 181 CTTTACAGCATCGCGCGCTCGCGCATTTTACGACTTCGACACCCCAATTCGCCCGTCAACCG 240  
 QY 298 TATCTCGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGGGCGAGCGACAGC 357  
 Db 241 TATCTCGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGGGCGAGCGACAGC 300  
 QY 358 TTACGCCAAACCTCCATCGCGCTCGCGGTATTGACGGGCGTAAAGCTATGCGGTTACCCCG 417  
 Db 301 TTACGCCAAACCTCCATCGCGCTCGCGGTATTGACGGGCGTAAAGCTATGCGGTTACCCCG 360  
 QY 418 AATGTCGATTTGGATCGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAA 477  
 Db 361 AATGTCGATTTGGATCGCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAA 420  
 QY 478 AACGTCGCTTCGCGGCAACTGTCCCGCGGCTCGCGCTCGCGCTCAAAATTCGA 525  
 Db 421 AACGTCGCTTCGCGGCAACTGTCCCGCGGCTCGCGCTCAAAATTCGA 468



RESULT 15

ID ABZ38960/c  
 XX ABZ38960 standard; DNA; 486 BP.

AC ABZ38960;

XX 07-MAR-2003 (first entry)

XX N. gonorrhoeae nucleotide sequence SEQ ID 2509.

XX Antibacterial; infection; vaccine; gene therapy; gene; ds.

XX Neisseria gonorrhoeae.

XX WO200279243-A2.

XX 10-OCT-2002.

XX 12-FEB-2002; 2002WO-IB002069.

XX 12-FEB-2001; 2001GB-00003424.

XX (CHIR-) CHIRON SPA.

XX Fontana MR, Pizza M, Masignani V, Monaci E;

XX WPI; 2003-058415/05.

XX P-PSDB; ABP77990.

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
 PT medicament for treating or preventing N. gonorrhoeae infection.

XX Disclosure; Page 371; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.  
 CC Also disclosed are the nucleic acid molecules encoding the proteins and  
 CC antibodies that specifically bind to the proteins. The composition  
 CC comprising the protein, nucleic acid or antibody is useful for the  
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
 CC infection, this may be in the form of a vaccine or gene therapy.  
 CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid  
 CC molecules of the invention

XX SQ Sequence 486 BP; 101 A; 107 C; 168 G; 110 T; 0 U; 0 Other;

Query Match 70.1%; Score 368; DB 10; Length 486;

Best Local Similarity 95.6%; Pred. No. 1e-84;

Matches 390; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 121 GGTCTGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 180

DB 486 GGTCTGCAAGGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAAGACCTCCGC 427

QY 181 TTGCGCGTCGATTACACGGCTACAAAACCTATA---AAGCCCATCCACCGATTTCAAA 237

DB 426 TTGCGCGTCGATTACACGGCTACAAAACCTATAAAAGCCCATCCACCGATTTCAAA 367

QY 238 CTTTACAGCATCGGCGGTTCGCCATTACGACTTCGACACCCAAATCGCCGTCMAACCG 297

DB 366 CTTTACAGCATCGGCGGTTCGCCATTACGACTTCGACACCCAAATCGCCGTCMAACCG 307

QY 298 TATCTCGGCGCGCTTCAGCCCTCAACCGCTCCGCTCGACTTGGGCGGCGACACAGC 357

DB 306 TATTTGGCGCGCGCTTCAGCCCTCAACCGCTTCGCCCTCCGCGGCGGCGACAGC 247

QY 358 TTCAGCCAAACCTCCATCGGCTTCGGCGTATTGACGGGTAAGCTATCGGTTACCCCG 417

DB 246 TTCAGCAAAACCTCCGCGGCTTCGGCGTATTGCGGGGTAAGCTATCGGTTACACCC 187

QY 418 AATGTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACTGTCAA 477

DB 186 AATGTCGATCTGGATGCCGGCTACCGCTACAACTACGTCCGCAAGTCAACAATGTCAA 127

QY 478 AACGTCCGTTCCCGCGGAACCTGTCCGTCCGGCTGCGCGTCAAAATTTCTGA 525

DB 126 AACGTCCGTTCCCGCGGAACCTGTCCGTCCGGCTGCGCGTCAAAATTTCTGA 79

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 Job time : 1070 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC  
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Searched: 1202784 seqs, 818139359 residues

Total number of hits satisfying chosen parameters: 2405568

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Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	518.6	98.8	850	3	US-08-913-362-5
3	502.6	95.7	810	3	US-08-913-362-7
4	501.2	95.5	528	3	US-08-913-362-29
5	491.2	93.6	710	3	US-08-913-362-3
6	49.8	9.5	1919	4	US-09-614-912-175
7	45.6	8.7	4403765	3	US-09-103-840A-2
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11	44	8.4	1082	4	US-09-881-165-4
12	44	8.4	4483	3	US-08-961-527-363
13	44	8.4	32768	3	US-08-961-527-71
14	43.6	8.3	390	3	US-09-197-649-7
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17	43	8.2	925	3	US-08-997-467-1
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24	42	8.0	1977	3	US-08-894-8188-6
25	42	8.0	1977	3	US-09-445-472-11
26	42	8.0	1977	4	US-10-090-624-11
27	41.6	7.9	867	4	US-09-216-393B-340

28	41.6	7.9	867	4	US-09-216-393B-342	Sequence 342, App
29	41.6	7.9	1397	4	US-09-216-393B-343	Sequence 343, App
c 30	41.6	7.9	1397	4	US-09-216-393B-345	Sequence 345, App
c 31	41.4	7.9	1614	4	US-09-489-039A-3484	Sequence 3484, Ap
32	41.4	7.9	1698	4	US-09-489-039A-3505	Sequence 3505, Ap
33	41.4	7.9	1706	4	US-10-033-109-3	Sequence 3, Appli
34	41.4	7.9	3486	4	US-09-614-221A-292	Sequence 292, App
35	41.4	7.9	25254	4	US-09-902-540-1233	Sequence 1233, Ap
36	41.2	7.8	1781	4	US-09-675-018B-7	Sequence 7, Appli
37	41.2	7.8	1889	4	US-09-675-018B-9	Sequence 9, Appli
c 38	41	7.8	1439	3	US-09-056-556-167	Sequence 167, App
c 39	41	7.8	1439	3	US-09-072-596-162	Sequence 162, App
c 40	41	7.8	1439	4	US-03-072-967-167	Sequence 167, App
41	40.8	7.8	822	3	US-09-228-986-38	Sequence 38, Appli
42	40.8	7.8	822	4	US-10-101-464A-38	Sequence 38, Appli
43	40.8	7.8	2138	4	US-10-101-464A-462	Sequence 462, App
44	40.8	7.8	7218	1	US-08-232-463-14	Sequence 14, Appl
45	40.6	7.7	435	4	US-09-252-991A-6817	Sequence 6817, Ap

ALIGNMENTS

RESULT 1  
US-08-913-362-1  
; Sequence 1, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913.362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406.362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001.983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 830 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 143..667
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 143..199
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; NAME/KEY: mat_peptide
; LOCATION: 200..667
;
US-08-913-362-1

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QY 1 ATGAAAAAGCACTTCCACACTGATTGGCTTCCCGCGCGCGCACTGGCGGAA 60
DB 143 ATGAAAAAGCACTTCCACACTGATTGGCTTCCCGCGCGCGCACTGGCGGAA 202

QY 61 GCGGCATCCGGCTTTTACGTCGAAGCGGATGCGGCACGCAAAAGCTCAAGCTCTTTA 120
DB 203 GCGGCATCCGGCTTTTACGTCGAAGCGGATGCGGCACGCAAAAGCTCAAGCTCTTTA 262

QY 121 GGTTCGCCAAAGGCTTCAGCCCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180
DB 263 GGTTCGCCAAAGGCTTCAGCCCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 322

QY 181 TTCCGCGTGTATACAGCGCTCAAAAACATAAAGCCCATCCACCGATTTCAAACTT 240
DB 323 TTCCGCGTGTATACAGCGCTCAAAAACATAAAGCCCATCCACCGATTTCAAACTT 382

QY 241 TACAGCATCGCGCGTCCGCAATTTACGACTTCGACACCCCAATCGCCCGTCAAAACGAT 300
DB 383 TACAGCATCGCGCGTCCGCAATTTACGACTTCGACACCCCAATCGCCCGTCAAAACGAT 442

QY 301 CTCGGCGCGGCTTGAGCCTTCAACCGCGCTCGCTCGACTTGGCGCGGCGACGACGTTTC 360
DB 443 CTCGGCGCGGCTTGAGCCTTCAACCGCGCTCGCTCGACTTGGCGCGGCGACGACGTTTC 502

QY 361 AGCAAACTCCATCGGCTTCGCGGATTTGACGGGCGTAACTATCGGTTACCCCGAAT 420
DB 503 AGCAAACTCCATCGGCTTCGCGGATTTGACGGGCGTAACTATCGGTTACCCCGAAT 562

QY 421 GTCGATTGTGATCCCGCTACCGCTCAACTACATCGCAAAAGTCAACACTGTCAAAAAC 480
DB 563 GTCGATTGTGATCCCGCTACCGCTCAACTACATCGCAAAAGTCAACACTGTCAAAAAC 622

QY 481 GTCGTTCCGGGAACTGTCCGTCGCGTCCGCTCAAAATTCGTA 525
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RESULT 2
US-08-913-362-5
; Sequence 5, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

```

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; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/913,362
; PRIORITY APPLICATION DATA:
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 08/406,362
; PRIORITY APPLICATION DATA:
; FILING DATE: 04-AUG-1995
; APPLICATION NUMBER: US 60/001,983
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: Z4063
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 208..732
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 208..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..732
;
US-08-913-362-5

Query Match      98.8%; Score 518.6; DB 3; Length 850;
Best Local Similarity 99.2%; Pred. No. 3e-136;
Matches 521; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGAAAAAGCACTTCCACACTGATTGGCTTCCCGCGCGCGCACTGGCGGAA 60
DB 208 ATGAAAAAGCACTTCCACACTGATTGGCTTCCCGCGCGCGCACTGGCGGAA 267

QY 61 GCGGCATCCGGCTTTTACGTCGAAGCGGATGCGGCACGCAAAAGCTCAAGCTCTTTA 120
DB 268 GCGGCATCCGGCTTTTACGTCGAAGCGGATGCGGCACGCAAAAGCTCAAGCTCTTTA 327

QY 121 GGTTCGCCAAAGGCTTCAGCCCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 180
DB 328 GGTTCGCCAAAGGCTTCAGCCCGCGCATCTCCGCGAGGCTACCGCATCAACGACCTCCGC 387

QY 181 TTCCGCGTGTATACAGCGCTCAAAAACATAAAGCCCATCCACCGATTTCAAACTT 240
DB 388 TTCCGCGTGTATACAGCGCTCAAAAACATAAAGCCCATCCACCGATTTCAAACTT 447

QY 241 TACAGCATCGCGCGTCCGCAATTTACGACTTCGACACCCCAATCGCCCGTCAAAACGAT 300
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DB 508 CTCGGCGCGGCTTGAGCCTTCAACCGCGCTCGCTCGACTTGGGGGCGGACGACGTTTC 567

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Qy 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
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Qy 481 GTCGTTCCGGGAACTGTCTCGTGGCGTGGCGGTCAAAATCTGA 525
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RESULT 3
US-08-913-362-7
; Sequence 7, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Neisseria gonorrhoeae
; STRAIN: b2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 241..765
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 241..297

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; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 298..765
US-08-913-362-7

Query Match 95.7%; Score 502.6; DB 3; Length 810;
Best Local Similarity 97.3%; Pred. No. 9.5e-132; Indels 0; Gaps 0;
Matches 511; Conservative 0; Mismatches 14;

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Qy 301 CTGCGCGCGCTTGAGCCTCAACCGCGCTTCGCGCTTCGCGCTTCGGCGGCGAGCAGCTTC 360
Db 541 TTGCGCGCGCTTGAGCCTCAACCGCGCTTCGCGCTTCGGCGGCGAGCAGCTTC 600
Qy 361 AGCAAACTCCATCGGCTCGGCGTATTGACGGGCGTAAGCTATGCGTTACCCCGAAT 420
Db 601 AGCAAACTCCGCGCGCTCGGCGTATTGCGGCGTAAGCTATGCGTTACCCCGAAT 660
Qy 421 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 480
Db 661 GTCGATTGGATGCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAAC 720
Qy 481 GTCGTTCCGGGAACTGTCTCGTGGCGTGGCGGTCAAAATCTGA 525
Db 721 GTCGTTCCGGGAACTGTCTCGTGGCGTGGCGGTCAAAATCTGA 765

```

```

RESULT 4
US-08-913-362-29
; Sequence 29, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997

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Db      296  |||||||TTCGCGCGTGCATATACGCGCTACAAAAAATATAAAGTCCCATCCACCGATTTCAA 355
Qy      238  CTTTACAGCATCGCGCGTCCGCGCATTTACGACTTCGACACCCCAATCGCCCGTCAAAACCG 297
Db      356  CTTTACAGCATCGCGCGTCCGCGCATTTACGACTTCGACACCCCAATCCCGCGTCAAAACCG 415
Qy      298  TATCTCGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGGGGGAGGAGCAGC 357
Db      416  TATCTCGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTTAAACGGGAGGAGCAGC 475
Qy      358  TTCAGCAAACTCATCGGCGCTGGCGTATTGAGCGGCGTAAGCTATGCGGTACCCCG 417
Db      476  TTCAGCAAACTCATCGGCGCTGGCGTATTGAGCGGCGTAAGCTATGCGGTACCCCG 535
Qy      418  AATGTCGATTTGGATGCGCGGTACCGCTACACTACACTACGCAAAAGTCAACACTGTCAA 477
Db      536  AATGTCGATTTGGATGCGCGGTACCGCTACACTACACTACGCAAAAGTCAACACTGTCAA 595
Qy      478  AACGTCGCTTCGCGGAACTGTGCGTCCGCGCGTGGCGGTCAAAATCTGA 525
Db      596  AATGTCGCTTCGCGGAACTGTGCGCGCGGTACGCGTCAAAATCTGA 643

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RESULT 6

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US-09-614-912-175
; Sequence 175, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 175
; LENGTH: 1919
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-614-912-175

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Query Match      9.5%; Score 49.8; DB 4; Length 1919;
Best Local Similarity 49.8%; Pred. No. 0.00035;
Matches 126; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy      125  CTGCCAAAGGCTTACGCGCGCATCTCGCGAGGCTACGCACTCAACGACTCCGCTTCG 184
Db      396  CGCGCTACCGCGCTTCCTCCACCATGGCGGACCCACCTGAGGAGCAACGCTACTCGC 455
Qy      185  CCGTCGATACAGCGCTTACAAAAAATATAAAGCCCAATCCACCGATTTCAAATTTACA 244

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Db      456  CCGTCGACCTCCAGTCCCTCTGCTTCTACTCCGGGCCCAAGACCAAGCCCAAGCTCAACA 515
Qy      245  GCATCGCGCGTTCGCGCATTTAGCACTTCGACACCCCAATCGCCGTCAAAACCGTATCTCG 304
Db      516  GCCTCGAGGAGTGCAGCCCGAGCTGCTCAAGAGCTTTGACCGGCTCGGGATCCCTCTCG 575
Qy      305  GCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGGGGGAGGAGCAGCAGCTTCAGCC 364
Db      576  GCGAGCAGAGCGGCTCTCCAACGTCGCGCGTCAAGCGCGCTCATCGACTCCACCTCCATCG 635
Qy      365  AAACCTCCATCGG 377
Db      636  CCACCACCCACCG 648

RESULT 7
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Query Match      8.7%; Score 45.6; DB 3; Length 4403765;
Best Local Similarity 44.6%; Pred. No. 0.094;
Matches 180; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

Qy      10  GCACCTGCGCACACTGATTGCGCTCTCCGCGCGCGCGCGCTGCGGGAAGGCGCATCC 69
Db      3731458  GCCGTTGCGCGCCTTGCGCGCGCGCGCGCTGCGGCGCGCTGCTGACGCGCGCGTT 3731517
Qy      70  GGCTTTTACGTCGAAGCGGATGCGCGACACGCAAAAGCCTCAAGCTCTTTAGTTCTGCC 129
Db      3731518  GCCCGCGCGCGCGCGCTTGCGCGCGCGCGCGCTTGCCTTCGGGGCGCTCCCGGACCGCC 3731577
Qy      130  AAAGCTTCAGCGCGCATCTCGCAGGCTACCGCATCAACGACCTCCGTTGCGCGTC 189
Db      3731578  GTAGCGCGCGTTGCGCGCGCGCGCGCAACCCAGTCTCGGAGACGCGCGCTTGCGCGCC 3731637
Qy      190  GATTACACGCGCTACAAAAAATAAAGACCCCATCCACCGATTTCAAACTTTACAGCATC 249
Db      3731638  GAGCGCGCGCTTGCGCGCTAAGGAATGCCGCGCGCGCGCTACCGCGCTT 3731697
Qy      250  GCGCGCTCCGCGCATTTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTATCTCGCGCG 309
Db      3731698  GCGCGCTTGCGCGCTTCCCGCGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3731757
Qy      310  CGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGGGGGAGGAGCAGCTTCAGCAAAAC 369
Db      3731758  GGCACCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3731817
Qy      370  TCCATCGCGCTCGCGCTATTGACGGGCGTAAAGCTATGCGCGTTAC 413
Db      3731818  GCCCGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3731861

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RESULT 8
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      8.7%; Score 45.6; DB 3; Length 4411529;
Best Local Similarity 44.6%; Pred. No. 0.095;
Matches 180; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 10 GCACCTTGCACACTGATTGCTCTCCCGGCGCGCGCACTGCGGAGCGCGCATCC 69
Db 3739165 GCGTTTGGCGCCCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3739224

QY 70 GGCTTTTACGTCCAAAGCGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 129
Db 3739225 GCGCGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3739284

QY 130 AAGGCTTACGCGCGCGGATCTCCGAGGCTACCGATCAAGACCTCCGCTTCCGCGTC 189
Db 3739285 GTAGCGCGCGGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3739344

QY 190 GATTACACGGCTTACAAAATAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 249
Db 3739345 GAGCGCGCGGTTCCGCGCTTAAAGAAATGCGGCGCGCGCGCGCGCGCGG 3739404

QY 250 GCGCGCTCCGCGGATTTACGACTTCGACCCCAATCGCGCGCGCGCGCGCGCGG 309
Db 3739405 GCGCGCTGCGCGCTTCCCGCGCGGATGCGCGCGCGCGCGCGCGCGCGCG 3739464

QY 310 CGCTTACGCTCAACCGCGCGCTCCGTCGACTTGGGCGGCGGCGGCGGCGGCGG 369
Db 3739465 GGCACCGCGCGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3739524

QY 370 TCCATCGGCTCGCGCTTATGACGGCGGTAAGCTATGCGGTTAC 413
Db 3739525 GCGCGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 3739568

RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      8.6%; Score 45; DB 3; Length 4403765;
Best Local Similarity 44.9%; Pred. No. 0.14;
Matches 171; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY 133 GGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGAGCTCCGCTTCCCGCTCGAT 192
Db 427071 GGCATCGGGCTGACCGCGGACGGCTTGTCCGGCTTCAGTCCCTGAACCTCCGGCGCGG 427012

QY 193 TACAGCGCTACAAAACATAAAGCCCATCCACCGATTTCAAACTTTACAGCATCGGC 252
Db 427011 AACACCGGTTTCTTCAACTCCGGCACCGCAACACCGGCTTGTTCACACTCCGGCACCGGC 426952

QY 253 GGTCCGCGCATTTACGACTTCGACACCCCAATCGCCCGTCAAAACCGTATCTCGCGCGCGC 312
Db 426951 AACACCGGCTTGTTCACACTCCGGCACCGGCAACGTCGGCATCGGCAACATGGGACCGGC 426892

QY 313 TTGAGCCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTCAGCCAAACCTCC 372
Db 426891 GCGTTCCGGCTCGGCTATCCGGCGACAGCCAGGTGGGCGATCGGCGCACTCGGC 426832

QY 373 ATCGCGCTCGGCGATTTACGCGGCGTAAGCTATGCGCTTACCCGAAATGTCGATTTGGAT 432
Db 426831 AGTTTCAACATCGGCTTGTTTAACTCGGGCGACCGCAATGTCGGCATCGGCAACTCGGC 426772

QY 433 GCGGCTACCGCTACAACTACATCGGCAAGTCAACACTGTCAAAACGTCGTTCCGCGC 492
Db 426771 ACCGCAACGTCGGCATCGGCAACACCGGCGCGGCAACACCGGCGCATCGGCAACGCGGC 426712

QY 493 GAACTGTCCGTGGGCGTGC 513
Db 426711 AACTACAAACCGGCTTGTCTC 426691

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RESULT 10
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

```

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Query Match      8.6%; Score 45; DB 3; Length 4411529;
Best Local Similarity 44.9%; Pred. No. 0.14;
Matches 171; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY 133 GGCTTCAGCCCGCGCATCTCCGAGGCTACCGCATCAACGAGCTCCGCTTCCCGCTCGAT 192
Db 426913 GGCATCTGCTGACCGCGGACGGCTTGTCCGGCTTCAGTCCCTGAACCTCCGGCGCGGC 426854

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193 TACAGCGCTACAAAACTATAAGCCCATCCACCGATTTCAAATTTTACAGCATCGGC 252  
 426853 AACACCGGTTTCTTCAACTCCGGCAGCCGCAACACCGGCTTGTTCAACTCCGGCAGCCGC 426794  
 253 GCGTCCGCGCTTTACGACTTCGACACCAATCCGCGCTCAACCGTATCTCGGCGCGGC 312  
 426793 AACACCGGCTTGTTCAACTCCGGCAGCCGCAACCGTATCTCGGCGCATCGGCACTCGGC 426734  
 313 TTGAGCCTCAACCGCGCTCCGTCGACTTGGGCGGCGAGCAGCTTTCAGCAAACTCC 372  
 426733 GGCTTCGGCGTCCGCTATCCGGAGAGCAGCAGTGGGCGGCACTCGGC 426674  
 373 ATCGGCTCCGCGTATTGACGGGCGTAAAGTATCGGTATCCCGAATGTGATTTGGAT 432  
 426673 AGTTTCAACATCGGCTTGTTCAACTCCGGCAGCCGCAATGTTCGCGCATCGGCACTCGGC 426614  
 433 GCGGCTACCGCTACAACTACATCGGCAAAAGTCAACACTGTCAAAACGCTCGTTCCGGC 492  
 426613 ACCGGCAACGTCCGATCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCA 426554  
 493 GAACTGTCCGTCGGCGTCCGC 513  
 426553 AACTACAACCGGCTTGTCTC 426533

RESULT 11  
 US-09-881-165-4  
 ; Sequence 4, Application US/09881165  
 ; Patent No. 6632930  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HOOD, ELIZABETH  
 ; APPLICANT: HOWARD, JOHN  
 ; APPLICANT: BAILEY, MICHELE  
 ; APPLICANT: GASTEL, FRANS VAN  
 ; APPLICANT: WANG, HUAMING  
 ; APPLICANT: WARD, MICHAEL  
 ; APPLICANT: WOODARD, SUSAN  
 ; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE  
 ; TITLE OF INVENTION: ENZYMES PRODUCED IN PLANTS  
 ; FILE REFERENCE: 10032R  
 ; CURRENT APPLICATION NUMBER: US/09/881,165  
 ; CURRENT FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: 60/211,732  
 ; PRIOR FILING DATE: 2000-06-15  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 1082  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding  
 ; OTHER INFORMATION: Organophosphate Hydrolase  
 US-09-881-165-4

Query Match 8.4%; Score 44; DB 4; Length 1082;  
 Best Local Similarity 46.0%; Pred. No. 0.012;  
 Matches 149; Conservative 0; Mismatches 175; Indels 0; Gaps 0;  
 31 CTCGCTCTCCGCGCGCGCTTCTTACGTTTCTGCAAGGCTTTCAGTCCAGCGCATC 90  
 522 CTCGTGCTCAAGGCGCGCGCGCTTCTTACGTTTCTGCAAGGCTTTCAGTCCAGCGCATC 581  
 91 GCGGACACGCAAAAGCTTCTTACGTTTCTGCAAGGCTTTCAGTCCAGCGCATC 150  
 582 ACCGCGGCTTCCAGCGCGAGCGGAGCAGCGGCGCGCATCTTTCAGTCCAGCGCATC 641  
 151 TCCGAGGCTACCGCATCAACGACCTCCGCTTTCGCGCTTTCAGTCCAGCGCATCAAAAC 210  
 642 TCCCGTCCGCGGTGTGATCGGCGCATCTCCGAGCAGCAGGACCTCTCTTACCTCACC 701  
 211 TATAAGGCCCATCCACCGATTTCAAACTTTTACAGCATCGGCGGTCCGCCATTTCAGCAG 270

702 GCCTCGCGCGCGCGCTTCTTACGTTTCTGCAAGGCTTTCAGTCCAGCGCATC 761  
 271 TTGACACCACTTCCGCGCGCTTTCAGTCCAGCGCATC 330  
 762 CTCGAGGACAAAGCTTCCGCGCGCTTCTTACGTTTCTGCAAGGCTTTCAGTCCAGCGCATC 821  
 331 TCGTTCGACTTGGGCGGCGAGCAGC 354  
 822 CTCCTCATCAAGCGCTTTCAGTCCAGCGCATC 845

RESULT 12  
 US-08-961-527-363  
 ; Sequence 363, Application US/08961527  
 ; Patent No. 6420135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles Kunsch  
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
 ; NUMBER OF SEQUENCES: 391  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: Maryland  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 ; COMPUTER: HP Vectra 486/33  
 ; OPERATING SYSTEM: MSDOS version 6.2  
 ; SOFTWARE: ASCII Text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/961,527  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Brookes, A. Anders  
 ; REGISTRATION NUMBER: 36,373  
 ; REFERENCE/DOCKET NUMBER: PB340P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (301) 309-8504  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 363:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4483 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 US-08-961-527-363

Query Match 8.4%; Score 44; DB 3; Length 4483;  
 Best Local Similarity 47.3%; Pred. No. 0.021;  
 Matches 174; Conservative 0; Mismatches 185; Indels 9; Gaps 1;  
 134 GCTTCAGCGCGCGCATCTCCGCGGCTTACGCGCATCAACGACCTCGGTTCCGCGCTCGATT 193  
 2659 GCTTCAGCGCGCATCAAGTGGCTTTCAGCATCAACGAGTGTTCAGTCTTTCAGTCTTTCAGTCT 2718  
 194 ACAGCGCGCTACAAAGCTTATAAGCGCGCGCATCAACGCGGCTTTCAGTCTTTCAGTCTTTCAGTCT 253  
 2719 ACCAGTGGCTTTCAGTCTTTCAGCATCAACGAGTGTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCT 2778  
 254 GGTCCGCGCATTTA-----CGACTTCGACACCGCATCCCGCGTTCMAACCGTATCTCG 304  
 2779 GCTTCAGCAAGTACTAGTGTGATCGGCTTTCAGCATCGACAGTGTCTTTCAGTCTTTCAGTCTTTCAGTCT 2838  
 305 GCGCGCGCTTTCAGCTCAACCGCGCGCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCT 364  
 2839 ACAGTGTCTTCGCGCTTTCAGCATCAACGAGTGTTCAGCTTTCAGTCTTTCAGTCTTTCAGTCTTTCAGTCT 2898

QY 365 AAACCTCCATCGGCTTCGGCGTATTGACGGGGTAAAGTATGCGGTATACCCGGAATGTGCG 424  
 Db 2899 GAATCTGCATCAACAGTGGTCCGCTTCAGCGTCAACAGTGGTTCGGCTTCAGGTCG 2958  
 QY 425 ATTGATGCGGCTACCGCTCAACTCACTCATCGGCAAGTCAACTGTCAAAAACGTCC 484  
 Db 2959 ACAAGTGTTCGGCTTCAGCATCAACAGTGGTTCGGCTTCAGCAAGCGCAAGTACCTCA 3018  
 QY 485 GTTCGGGC 492  
 Db 3019 GGTTCAGC 3026

RESULT 13  
 US-08-961-527-71  
 ; Sequence 71, Application US/08961527  
 ; Patent No. 6420135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles Kunsch  
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
 ; NUMBER OF SEQUENCES: 391  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: Maryland  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 ; COMPUTER: HP Vectra 486/33  
 ; OPERATING SYSTEM: MSDOS version 6.2  
 ; SOFTWARE: ASCII Text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/961,527  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Brookes, A. Anders  
 ; REGISTRATION NUMBER: 36,373  
 ; REFERENCE/DOCKET NUMBER: PB340P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (301) 309-8504  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 71:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 32768 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; US-08-961-527-71

Query Match 8.4%; Score 44; DB 3; Length 32768;  
 Best Local Similarity 47.3%; Pred. No. 0.043;  
 Matches 174; Conservative 0; Mismatches 185; Indels 9; Gaps 1;  
 QY 134 GCTTACGCGCGCATCTCGGAGGCTACCGAGTCAACGACCTCCGCTTCGGCGTGGATT 193  
 Db 1442 GTTTCAGCAAGTACCAAGTGGTTCAGCATCAACAGTGGTTCAGTCTCAGCGTCA 1501  
 QY 194 ACAGCGGCTACAAAACATAAAGCCCCATCAACGATTTCAAACATTTACAGCATCGGG 253  
 Db 1502 ACCAGTGCCTCAATCAGCATCAACAGTGGCTTCAGCAAGCAACAGTGGTGG 1561  
 QY 254 CGTCCGCCATTTA-----CGACTTCGACACCAATCGCCCGTCAAAACCGTATCTCG 304  
 Db 1562 GCTTCAGCAAGTACTAGTGCATCGGCTTCAGCATCGACAAGTGGTCTGAATCGGGCATCA 1621  
 QY 305 GCGCGGCTTGAGCTCAACCGCGCTTCGTCGACTTGGGGCGCAGCAGCTTCAGCC 364

Db 1622 ACAGTGTCTCGCTTCAGCATCAACAGTGGTTCAGCTCAGCAAGCAGCATCAGCTTCT 1681  
 QY 365 AAACCTCCATCGGCTTCGGCGTATTGACGGGGTAAAGTATGCGGTATACCCGGAATGTGCG 424  
 Db 1682 GAATCTGCATCAACAGTGGTCCGCTTCAGCGTCAACAGTGGTTCGGCTTCAGGTCG 1741  
 QY 425 ATTGATGCGGCTACCGCTCAACTCACTCATCGGCAAGTCAACTGTCAAAAACGTCC 484  
 Db 1742 ACAAGTGTCTCGCTTCAGCATCAACAGTGGTTCGGCTTCAGCAAGCGCAAGTACCTCA 1801  
 QY 485 GTTCGGGC 492  
 Db 1802 GGTTCAGC 1809

RESULT 14  
 US-09-197-649-7  
 ; Sequence 7, Application US/09197649  
 ; Patent No. 6194550  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gold, Larry  
 ; APPLICANT: Tuerk, Craig  
 ; APPLICANT: Pribrnow, David  
 ; APPLICANT: Smith, Jonathan D.  
 ; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation  
 ; FILE REFERENCE: NEX02/C1-CON  
 ; CURRENT APPLICATION NUMBER: US/09/197,649  
 ; CURRENT FILING DATE: 1998-11-23  
 ; EARLIER APPLICATION NUMBER: 07/829,461  
 ; EARLIER FILING DATE: 1992-01-31  
 ; EARLIER APPLICATION NUMBER: 07/739,055  
 ; EARLIER FILING DATE: 1991-08-01  
 ; EARLIER APPLICATION NUMBER: 07/561,968  
 ; EARLIER FILING DATE: 1990-08-02  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 390  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Sequence  
 ; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed  
 ; OTHER INFORMATION: fragments having NcoI restriction sites.  
 ; US-09-197-649-7

Query Match 8.3%; Score 43.6; DB 3; Length 390;  
 Best Local Similarity 45.0%; Pred. No. 0.011;  
 Matches 163; Conservative 0; Mismatches 199; Indels 0; Gaps 0;  
 QY 147 CATCTCCGAGGCTACCGCATCAACGAGCTTCGGCTTCGGCGTATTACACGCGTACAA 206  
 Db 5 CATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 64  
 QY 207 AAACCTATAAGCCCATCCACCGATTTCAAATTTTACAGCATTCGGCGGTTCGGCATTTA 266  
 Db 65 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 124  
 QY 267 CGACTTCGACACCCCAATCGCCGTCAAACCGTATCTTCGGCGCGCTTCGAGCTCAACCG 326  
 Db 125 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 184  
 QY 327 CGCTCTCCGCTTCGACTTGGGGCGGACGACGAGTTCAGCCAAACCTCCATCGGCTTCGGGT 386  
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 QY 387 ATTGACGGGCTGAAGTATGCGTTACCCGGAATGTCGATTTGGATGCGGGTACCGCTA 446  
 Db 245 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 304  
 QY 447 CAACTACATCGCAAGTCAACACTGTCAAAAACGTCGTTCCGGCGCACTGTCTCGTGG 506



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 13:08:07 ; Search time 7695 Seconds  
(without alignments)  
2596.977 Million cell updates/sec

Title: US-10-650-123-1

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_ges1:\*
- 9: gb\_ges2:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	56.4	10.7	626	6	CA193415 SCCFL100
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4	53.6	10.2	591	6	CB640993 OSJNEA17F
5	53.6	10.2	665	7	CV152413 LS245-S-S
6	53.6	10.2	698	6	CB653730 OSJNEC05A
7	53.6	10.2	725	6	CB677411 OSJNEE14E
8	53.6	10.2	741	7	CF589226 EST00F06
9	53.6	10.2	759	6	CB671800 OSJNEE05I
10	53.6	10.2	762	6	CB677339 OSJNEE14C
11	53.6	10.2	775	6	CB677062 OSJNEE13K
12	53.6	10.2	778	6	CB654692 OSJNEC07G
13	53.6	10.2	782	6	CB665147 OSJNEE11F
14	53.6	10.2	842	6	CB668023 OSJNEE15K
15	53.4	10.2	561	7	CF278525 14ETL--04
16	53.4	10.2	644	7	CF315326 HD--04-D0
17	52.2	9.9	525	7	CF308604 ABF--02-H
18	52	9.9	696	6	CD935542 OV.101M15
19	51.8	9.9	530	7	CF335206 JMT--04-M
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21	51.8	9.9	655	6	CA172233 SCSPB107
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40	48.8	9.3	567	2	BE593027	BE593027	WSL_93_D1
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ALIGNMENTS

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DEFINITION 5', mRNA sequence.  
ACCESSION CA197724  
VERSION CA197724.1 GI:35228269  
KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.  
REFERENCE 1 (bases 1 to 622)  
Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: paruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 074 row: C column: 04  
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/clone\_lib="AD1"  
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[seedlings inoculated with Gluconacetobacter  
diaetotrophicans]. cDNA was prepared from polyA+ mRNA using  
SuperScript Plasmid System Kit (Invitrogen). The  
double-strand cDNAs were fractionated in a sepharose  
CL-2B 40cm-column and fragments sizing between 0.8 and  
1.5 Kb were directionally cloned into the vector. Details

FEATURES  
source

of each source of RNA and library construction can be obtained at <http://sucet.lad.ic.unicamp.br/public>

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ORIGIN
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Best Local Similarity 47.4%; Pred. No. 4.3e-05;
Matches 173; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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Db 108 TGATCGCTCTCGGATCGCATCAATTCACCGCGGCGAGTCCCGGTGACGCCGACG 167

QY 87 CGATCGCGACACGCAAAAGCCTCAAGCTCTTTAGTTTCGCAAAAGGCTTCAGCCCGCG 146
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QY 147 CATCTCGGAGGTACCGCATCAACGCTCCGCTTCGCGCTGATTAACGGCTACAA 206
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QY 207 AAATATAAGCCCATCCACCGATTCAAACTTTACAGCATCGGCGCGTCCGCCATTTA 266
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QY 267 CGACTTCGACACCAATCGCCGCTCAAAACGTAATCTCGGCGCGCTTTAGGCTCAACCG 326
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Db 348 CTTCTCAGCGCCACACGCGCTCTCCGTCACCGTCGCGGAGCGCGCTACCGGTCCTCA 407

QY 327 CGCTCGCTGACTTGGGCGGACGACAGCTTCAGCCAACTCATCGGCTCGGCT 386
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Db 408 CCACTCGCTGACGTCTCCCGCGTGAGCCCGACACCGGTCCCGGACCCCTTCGCCGT 467

QY 387 ATTGA 391
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Db 468 CTTCA 472

RESULT 2
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LOCUS SCCCF1003B05.g FL1 Saccharum officinarum cDNA clone SCCCF1003B05
5', mRNA sequence.
CA193415
VERSION CA193415.1 GI:35140555
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 626)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 003 row: E column: 05
Seq primer: T7 Promoter Primer.
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DEFINITION
CA193415
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
CA193415 787 bp mRNA linear EST 09-APR-2003
OSJNEC07F21.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC07F21 5', mRNA sequence.
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ACCESSION CB654660
VERSION CB654660.1 GI:29658385
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 787)
AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
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Fax: 520 621 9288  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: gta aac cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
Plate: 07 row: F column: 21  
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Best Local Similarity 44.7%; Pred. No. 0.00023; Mismatches 263; Indels 0; Gaps 0;  
Matches 213; Conservative 0; Mismatches 263; Indels 0; Gaps 0;  
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QY 101 CAAAGCCTCAAGCTCTTTAGTTTGTGCAAGGTTTCAGCCCGCGCATCTCCGAGGCT 160  
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DB 360 TCCCGCTCGACAAACAAACAAACAAAGTCTACGCGCGCGCGCGCGCGCGCGCGCG 419  
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DB 420 ACAAGTCAACGCTTCGGGTTCAAGATGCGGGGTTTACAAACAGCAGCAACGCGG 479  
QY 461 AAGTCAACACTGTCAAAACGTCCTTCGCGGAACTGTTCGCGTTCGCGTTCGCGCTC 516  
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LOCUS  
DEFINITION  
clone OSJNE07F21 5', mRNA sequence.  
ACCESSION  
CB640993  
VERSION  
CB640993.1  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa (japonica cultivar-group)  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE  
1 (bases 1 to 591)

AUTHORS  
Jantaauriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,  
Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.  
Large-scale identification of ESTs involved in the interaction  
between rice and Magnaporthe grisea  
Unpublished (2003)  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: atc agc ggc cgc gat cc  
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Plate: 17 row: F column: 21  
Seq primer: atc agc ggc cgc gat cc.  
Location/Qualifiers  
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DB 336 TCCCGCTCGACAAACAAACAAACAAAGTCTTACGCGCGCGCGCGCGCGCGCGCG 395  
QY 401 GCTATCGCGTTACCGCGAATGTCGATTTGGATGCGCGGCTTACCGCTACCACTACATCGGCA 460  
DB 396 ACAAGTCAACGCTTCGGGTTCAAGATGCGGGGTTTACAAACAGCAGCAACGCGG 455  
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ACCESSION   CB677411
VERSION     CB677411.1 GI:29681136
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 725)
AUTHORS    Jantassuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE      Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
JOURNAL    Unpublished (2003)
COMMENT    Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: E column: 24
Seq primer: gta aaa cga cgg cca gtc.
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XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

Query Match      10.2%; Score 53.6; DB 6; Length 725;
Best Local Similarity 44.5%; Pred. No. 0.00064;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

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Qy      101 CAAAAGCCTCAAGCTCTTTAGTCTTTCGCAAAAGGCTTCAGCCCGCGATCTCCGAGGCT 160
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Qy      281 AATCGCGGTCAAACCGTATCTCGCGCGCGCTTGAGCCTCAACGCGGCTCCGTCGACT 340
Db      262 TCGGCTCGGCAAGCTCGCCTTCGCGCGCACCAAGGCGGACCGGTACAAACAGCGTCAACC 321
Qy      341 TGGCGCGGACGAGCAGCTTCAGCCAAACCTCATCTCGGCTCGGGGTATTTGACGGCGGTAA 400
Db      322 TCCCGGTGACAAACAACAACAAGTCTACGCGGCGCGCCCAAGATCAACAACA 381
Qy      401 GCTATGCGGTTACCCGAATGTCGATTTGGATGCGCGCTACCGTACAACTACATCGGCA 460
Db      382 ACAAGCTCAACGCCTTCGCGGTTCAACAAGATGCGGGTTACAACAACAGCAGCAACGGCG 441
Qy      461 AAGTCAACACTGTCAAAACGTCGTTCCGCGGGAACACTGTCGTCGCGGTCGCGTC 516
Db      442 GCGGCAACTACGCGGCAACGCGCGCGACGCTGTAAGAGCTACTTCAACAAGTTCGTC 497

RESULT 8
LOCUS   CF589226
DEFINITION   EST00F06 Subtracted cDNA library of JA/BTH-treated rice leaf Oryza
            sativa (japonica cultivar-group) cDNA clone JBI93, mRNA sequence.
ACCESSION   CF589226
VERSION     CF589226.1 GI:36355281
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 741)
AUTHORS    Yang,Y.
TITLE      Subtracted cDNA library of JA/BTH-treated rice leaf
JOURNAL    Unpublished (2003)
COMMENT    Contact: Yinong Yang
            Plant Pathology Department
            University of Arkansas
            217 Plant Sci Bldg, Fayetteville, AR 72701, USA
            Tel: 501-575-5635
            Fax: 501 575 7601
            Email: Yiyang@uark.edu
            Seq primer: T7
            Location/Qualifiers
             1..741
             /organism="Oryza sativa (japonica cultivar-group)"
             /mol_type="mRNA"
             /cultivar="Drew (a major cultivated variety in Arkansas)"
             /db_xref="taxon:39947"
             /clone="JBI93"
             /tissue_type="Seedling leaves"
             /dev_stage="16-day-old rice seedling treated by JA/BTH"
             /clone_lib="Subtracted cDNA library of JA/BTH-treated rice
             leaf"
             /note="Vector: pGEM-T easy; Rice seedling leaves were
             pretreated with 0.3 mM cycloheximide (CHX) half an hour
             before treatment of 0.2 mM jasmonic acid (JA) or 0.4 mM
             benzoethiadiazole (BTH). Both JA- and BTH-induced mRNAs
             were equally pooled for subtracted cDNA library
             construction"

ORIGIN

Query Match      10.2%; Score 53.6; DB 7; Length 741;
Best Local Similarity 44.5%; Pred. No. 0.00064;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

Qy      41 CGCGCGCGCACTGCGGGAAGCGCATCGCGCTTTTACGTCCAAAGCGATCGGCACACG 100

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Seq primer: gta aaa cga cgg cca gtc.			
Location/Qualifiers			
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/organism="Oryza sativa (japonica cultivar-group)"			
/mol_type="mRNA"			
/cultivar="Nipponbare"			
/db_xref="taxon:39947"			
/clone="OSUNBE14C19"			
/tissue_type="Leaf"			
/dev_stage="3 week"			
/lab_host="DH10B"			
/clone_lib="OSJNBe"			
/note="Vector: pluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 24 hrs after inoculation with Rice Blast (70-15)"			
ORIGIN			
Query Match 10.2%; Score 53.6; DB 6; Length 762;			
Best Local Similarity 44.5%; Pred. No. 0.00065;			
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;			
Qy	41	CGGCCGCGCACTCGCGGAAGCGCATCCGGCTTTTACGTCCAAGCCGATCCGCACACG	100
Db	33	CAGCAGCGGCATCGAGGATACGACCGGAGTTCTACCACTTCAGCGACCACTGCGGC	92
Qy	101	CAAAAGCCTCAAGCTCTTTAGTTCTGCGAAAGGCTTCAGCCCGGCATCTCCGAGCT	160
Db	93	TGCAGACGGCGAGCTTCTCGGCGCTCTCCCTCGGCGACTCCATCTGGTCTCTCCCTCCG	152
Qy	161	ACGSCATCAAGACCTCGCTTCGCGTTCGATTACACGCGCTACAAAACCTATAAGCC	220
Db	153	ACGCCGCAAGCAGCGGCTTCGACGGGAGTACCACTTCTCTCCCTCCCTCCCG	212
Qy	221	CATCCACCGATTTCAAACTTTACAGCATTCGGCGGCTCGCCCATTTACGACTTCGACACCC	280
Db	213	CCAGAAGCGCATCGCAACATCAACGGCGTCGCGGAACCTGGATGGCCCGGCTCA	272
Qy	281	AATCGCGCGTCAACCGTATCTCGGCGCGCTTTAGCCTCAACCGCGCTTCGCTCGACT	340
Db	273	TCGGCTCCGGCAAGCTCGCCTTCGCGCGCACCAAGGCGACCGCTACACAGCGTCAACC	332
Qy	341	TGGCGCGCAGCAGCTTCAGCCAAACCTCATCGCGCTCGGCGTATTGACGGGCGTAA	400
Db	333	TCGCCGTGCGACCAACAACAACAAAGTCTTACGGCGCGCGCCCAAGATCAACAACA	392
Qy	401	GCTATGCGGTTACCCCGAATGTCGATTGGATGCGGCTACCGCTACAACTACATCGCA	460
Db	393	ACAAGTCAAGCCCTTCGGGTTCAACAGATGGGGGTTACAAACAAGACGACGCGG	452
Qy	461	AAGTCAACACTGTCAAAACCTCGTTCGCGCGAACTGTCGTCGGCGTGGCGGTC	516
Db	453	CGCGCAACTACGGCGGCAACCGCGCGACGTTGAAGAGCTACTTCAACAAGTCGGTC	508
RESULT 11			
CB677062			
LOCUS			
DEFINITION			
OSJNBE13K18.f OSJNBe Oryza sativa (japonica cultivar-group) cDNA			
clone OSJNBE13K18 5', mRNA sequence.			
CB677062			
CB677062.1 GI:29680787			
EST.			
Oryza sativa (japonica cultivar-group)			
Oryza sativa (japonica cultivar-group)			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
Ehrhartoideae; Oryzeae; Oryza.			
1 (bases 1 to 775)			
Jantaariyavat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,			
Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.			
Large-scale identification of ESTs involved in the interaction			
between rice and Magnaporthe grisea			
Unpublished (2003)			
Contact: Rod Wing			
COMMENT			

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ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS      Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
              Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE        Large-scale identification of ESTs involved in the interaction
              between rice and Magnaporthe grisea
JOURNAL      Unpublished (2003)
COMMENT      Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
PCR PRIMERS  FORWARD: gta aaa cga cgg cca gtg
              BACKWARD: gga aac agc tat gac cat g
              Plate: 07 row: G column: 20
              Seq primer: gta aaa cga cgg cca gtg.

FEATURES
source      Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSUNEC07G20"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSUNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match      10.2%; Score 53.6; DB 6; Length 778;
Best Local Similarity 44.5%; Pred. No. 0.00065;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 41 CGGCCCGCAGCTTCGGCGGAGGCGCATCCGGCTTTTACGTCCAAAGCGGATCGGCACACG 100
Db 48 CAGCAGCGGCATGGAGGATACGACCGCGAGTTCTACCAAGTTTCAGCGACCAAGCTCGGC 107
QY 101 CAAAGCCTCAAGCTTTTAAAGTTCTGCCAAAGGCTTCAGCCGCGCATCTCGCAGGCT 160
Db 108 TGCAGACGGGAGCTTCTCGGCTCTCCCTCGGCGACTTCATCTGTGCTCTCCCTCCG 167
QY 161 ACCGCATCAACGACCTTCGCTTCGCGTCGATTACACGGGCTACAAAACCTATAAGCCC 220
Db 168 ACCGCGCAACGAGCGCGCTTCGACGGGAGTACCACCACTTCTCCTCCCTCCCG 227
QY 221 CATCCACGATTTCAAACTTTACAGATCGGCGGTCGCGCATTTAGCACTTCGACACCC 280
Db 228 CCAAGAACGCGATCGCAACATCAACGGGTCGCCGGAACCTTGGATGCCCGGCTCA 287
QY 281 AATCGCCGCTCAACACGCTATCTCGGCGCGCTTTCAGCGCTCAACCGCGCTTCGTCGACT 340
Db 288 TCGGCTCCGGCAAGCTCGCGCTTCGGCGCCACCAAGCGCGACCGCTACACAGGCTCAAC 347
QY 341 TGGCGCGCAGCGACGCTTCAGCAAACTTCATCGGCTTCGCGCTTCGCGGCTAAGCGGCTAA 400
Db 348 TCCCGCTCGACAAACAAACAAACAAAGTCTTACGCGCGCGCGCCAAAGATCAACAA 407
QY 401 GCTATCGGCTTACCCGAATGTCATTTGGATCGCGCTACCGCTACCACTACATCGCA 460
Db 408 ACAACGTCAACGCTTCGCGTTTCAACAGATGGGGGTTTACAAACAGCAGCAACGCGG 467
QY 461 AAGTCAACACTGTCAAAAACGTCCTTCGGCGCAACTGTTCGCGCGGCTCGCGGTC 516
Db 468 GCGGCACTACTCGGCGGCAACGGGCGGCGAGCTGAGAGCTACTTCAACAGTCTGTC 523

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## RESULT 13

CB665147  
LOCUS 782 bp mRNA linear EST 09-APR-2003  
DEFINITION OSUNED11F07.f OSJNED Oryza sativa (japonica cultivar-group) cDNA  
clone OSUNED11F07 5', mRNA sequence.

## ACCESSION

CB665147  
VERSION CB665147.1 GI:29668872

## KEYWORDS

EST.

## SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; Liliopsida;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 782)

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,

Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu

PCR PRIMERS

FORWARD: gta aaa cga cgg cca gtg

BACKWARD: gga aac agc tat gac cat g

Plate: 11 row: F column: 07

Seq primer: gta aaa cga cgg cca gtg.

Location/Qualifiers

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/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="OSUNED11F07"

/tissue\_type="Leaf"

/dev\_stage="3 week"

/lab\_host="DH10B"

/clone\_lib="OSJNEQ"

/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:

XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

Query Match 10.2%; Score 53.6; DB 6; Length 782;

Best Local Similarity 44.5%; Pred. No. 0.00065;

Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 41 CGGCCCGCAGCTTCGGCGGAGGCGCATCCGGCTTTTACGTCCAAAGCGGATCGGCACACG 100

Db 38 CAGCAGCGGCATGGAGGATACGACCGCGAGTTCTACCAAGTTTCAGCGACCAAGCTCGGC 97

QY 101 CAAAGCCTCAAGCTTTTAAAGTTCTGCCAAAGGCTTCAGCCGCGCATCTCGCAGGCT 160

Db 98 TGCAGACGGGAGCTTCTCGGCTCTCCCTCGGCGACTTCATCTGTGCTCTCCCTCCG 157

QY 161 ACCGNTCAACGACCTTCGCTTCGCGTCGATTACACGGGCTACAAAGGCTATAAGCCC 220

Db 158 ACCGCGCAACGAGCGCGCTTCGACGGGAGTACCACCACTTCTCCTCCCTCCCG 217

QY 221 CATTCACCGATTTTAAACTTTTACAGCATCGGCGCGTTCGCCCATTTACGACTTCGACACCC 280

Db 218 CCAAGAACGCGATCGCAACATCAACGGGCTCGCGGAACCTTGGATGCCCGGCTCA 277

QY 281 AATCGCCGCTCAACCGGTATCTCGGCGCGGCTTTAGCTGCTCAACCGCGCTTCGTCGACT 340

Db 278 TCGGCTCCGCGAAGCTTCGCTTCGCGCGCCACCAAGGCGCGCTACAAACAGGCTCAACC 337

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QY 341 TGGGGCGGAGGAGCAGCTTACGCCAAACCTCATCGGCTCGCGGTATTGACGGCGGTAA 400
DB 338 TCCCGCTGCACAAACAAACAAAGTCTACCGGGCGCGCCCAAGATCAACAACA 397
QY 401 GCTATGCGGTTACCCGGAATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCA 460
DB 398 ACAAGCTCAAGCCCTTCGGGTTCAAGAATGCGGGGTTTACAACAACAGCAGCAACGGCG 457
QY 461 AAGTCAACACTGTCAAAACGTCCTGTCGGCGGAACCTGTCTCGTTCGGGCTGCGGCTC 516
DB 458 GCGGCAACTACCGCGCAACGCGCGGCGAGCTGTAAGAGTACTTCAACAAGTCGGTC 513

RESULT 14
LOCUS CB668023 842 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNEd15K14.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA
ACCESSION CB668023
VERSION OSJNEd15K14.5, mRNA sequence.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: K column: 14
Seq primer: gta aaa cga cgg cca gtc.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEd"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

Query Match 10.2%; Score 53.6; DB 6; Length 842;
Best Local Similarity 44.5%; Pred. No. 0.00065;
Matches 212; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 41 CGGCGCGCAGCTGCGGGAAGCGCATCCGGGTTTACGTCCAGCCGATCCGACACG 100
DB 42 CAGCAGCGCCATGGAGGATACGACCGCGAGTCTTACAGTTACGCGCAGCTGCGGC 101
QY 101 CAAAGCCTCAAGCTCTTTAGTTCTTGCCAAAGGCTTCAGCGCGGCATCTCCGAGGCT 160
DB 102 TGCAGACGGGAGCTTCTCCGCGCTCTCCCTCGGCGACTTCATCTGGTCTCTCCCTCCG 161
QY 161 ACCGATCAACGACCTCGCTTCGCGCTTCGATTAACACGCGCTACAAAAAATAAAGCCC 220

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DB 162 ACCGCGCAACGAGCGGCTTTCGACGGCGAGTACCACACTTCTCTCTCCCTCCCGG 221
QY 221 CATCCACGATTTCAAACTTTACAGCATCGGCGGTCCGCATTTACGACTTCGACACCC 280
DB 222 CAAGAAGCCCATCGCCAAACATCAACGCGCTCGCCGGAACCTGGATGGCCGCGCTCA 281
QY 281 AATCGCCCGTCAAAACCGTATCTCGGCGCGCGCTTTCGAGCTCAACCGCGCTCCGTCGACT 340
DB 282 TCGGCTCGGCAAGCTCGCCTTCGGCGCCACCAAGGCGGACCGCTTACAACGCGTCAACC 341
QY 341 TGGGGCGGAGGAGCAGCTTACGCCAAACCTCATCGGCTCGCGGTATTGACGGCGGTAA 400
DB 342 TCCCGCTGCACAAACAAACAAAGTCTTACGCGCGCGCGCCCAAGATCAACAACA 401
QY 401 GCTATGCGGTTACCCGGAATGTCGATTTGGATGCGGCTACCGCTACAACTACATCGGCA 460
DB 402 ACAAGCTCAAGCCCTTCGGGTTCAAGAATGCGGGGTTTACAACAACAGCAGCAACGGCG 461
QY 461 AAGTCAACACTGTCAAAACGTCCTGTCGGCGGAACCTGTCTCGTTCGGGCTGCGGCTC 516
DB 462 GCGGCAACTACCGCGCAACGCGCGGCGAGCTACTTCAACAAGTCGGTC 517

RESULT 15
LOCUS CF278525 561 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--04-H12.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-H12,
mRNA sequence.
ACCESSION CF278525
VERSION CF278525.1 GI:33655911
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1. 561
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 10.2%; Score 53.4; DB 7; Length 561;
Best Local Similarity 44.6%; Pred. No. 0.00071;
Matches 210; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

QY 41 CGGCGCGCAGCTGCGGGAAGCGCATCCGGGTTTACGTCCAGCCGATCCGACACG 100

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Db      71  CAGCAGCGCCCATGAGGGGATACGACCGGAGTTCTACCAAGTTACGACCAAGCTGCGGC 130
QY      101  CAAAAGCCTCAAGCTTTTAGGTTCTGCCAAAGGTTTCAGCCCGCGCATCTCCGCGAGCT 160
Db      131  TCGAGCGGCGAGCTTCTCCGGCCTCTCCCTCGGGACTCCATCTGGTCTCTCCCTCCG 190
QY      161  ACCGATCAACGACCTTCGCTTCGCGCTGATTACACGCGCTACAAAACCTATAAAGCCC 220
Db      191  ACCGCGCAACGACCGGCTTCGACGGGAGTACCACACTTCTCTCCCTCCGCG 250
QY      221  CATCCACCGATTTCAAACTTTACAGATCGGCGGCTCGGCATTTACGACTTCGACACCC 280
Db      251  CCAAGAACGCCATCGCCAAACATCAACGGGCTCGCCGGAACCTGGATGGCCCGGCCCTCA 310
QY      281  AATCGCCCGTCAACCGTATCTCGGCGGCGCTTGAGCCTCAACCGCGCTCCGTCGACT 340
Db      311  TCGGCTCCGGCAAGCTCGGCTTCGGGCGCCACCAAGGCGACCGCTACACAGCGTCAACC 370
QY      341  TGGGCGGCGACGACAGCTTCAGCCAAACCTCCATCGGCTTCGGCGTATTGACGGGCGTAA 400
Db      371  TCCCGTTCGACAAACAAACAAAGTCTTACGGGCGCGCCCAAGATCAACAACA 430
QY      401  GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGCTACCGCTACACTACATCGGCA 460
Db      431  ACAACGTCAACGCTTCGGGTTCAACAGATGGGGGTTTACAAACACAGCAGCAACGGCG 490
QY      461  AAGTCAACACTGTCAAAAACGTCGTTCCGGGGAACGTCCGTCGGCGTGC 511
Db      491  GCGGCAACGGCGGCGACGTGAGAGCTACTTCAACAAGTCGTCGGGAGGC 541

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Search completed: May 19, 2005, 19:31:26  
 Job time : 7711 secs

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2	868	100.0	174	6	ABU79079	Abu79079 N. mening
3	868	100.0	174	7	ADF43316	Adf43316 N. mening
4	868	100.0	174	8	ADL16114	Adl16114 Neisseria
5	868	100.0	174	8	ADL13428	Adl13428 Neisseria
6	868	100.0	174	8	ADL124352	Adl124352 N. meningi
7	864	99.5	174	8	ADP08236	Adp08236 Neisseria
8	857	98.7	174	8	ADL24383	Adl24383 N. meningi
9	854	98.4	174	2	AAW04893	AAW04893 Proteinase
10	825	95.0	174	2	AAW04894	AAW04894 Proteinase
11	825	95.0	174	5	ABG91063	Abg91063 Neisseria
12	824.5	95.0	175	2	AAW04892	AAW04892 Proteinase
13	820	94.5	166	8	ADL24385	Adl24385 N. meningi
14	809.5	93.3	162	6	ABP77991	Abp77991 N. gonorr
15	794	91.5	175	6	ADL24387	Adl24387 N. meningi
16	793	91.4	162	8	ADL24386	Adl24386 N. meningi
17	785	90.4	155	4	ABL19895	AbL19895 Neisseria
18	781	90.0	155	8	ADL13426	AdL13426 Neisseria
19	779.5	89.8	161	8	ADL24384	Adl24384 N. meningi
20	746	85.9	154	8	ADL24388	Adl24388 N. meningi
21	657.5	75.7	141	8	ADL24389	Adl24389 N. meningi
22	234	27.0	208	5	AAO17579	AAo17579 M. catarrh
23	224	25.8	232	6	ABP79561	Abp79561 N. gonorr
24	221.5	25.5	176	5	AAU97605	Aau97605 Haemophil
25	221.5	25.5	176	5	AAU97603	Aau97603 Haemophil

CC	humans. The antibodies may also be used diagnostically to detect N.	CC	sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC	meningitidis infection. The antigen may also be used to detect antibodies	CC	deleted), a construct useful in the treatment of cancer comprising a
CC	specific to N. meningitidis antigen. DNA sequences encoding the antigen,	CC	superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
CC	or their fragments, can be used as probes for the detection of pathogenic	CC	useful in the treatment of cancer (where an adaptor protein which
CC	Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)	CC	inhibits T cell activation by tumour associated antigens is deleted or
XX		CC	functionally deactivated), a composition useful in the treatment of
SQ	Sequence 174 AA;	CC	cancer (comprising a lipid raft conjugated to a superantigen), producing
	Query Match 100.0%; Score 868; DB 2; Length 174;	CC	(M2) a tumouricidal immunocyte population ex vivo in a mammal (by
	Best Local Similarity 100.0%; Pred. No. 9.3e-87;	CC	allowing tumour associated lipids to contact immunocytes, in which
	Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	receptors for the lipids are inactivated or deleted to produce a
		CC	tumouricidal immunocyte population, and administering the tumouricidally
QY	1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60	CC	activated immunocytes to the host), producing (M3) a tumouricidal APC
Db	1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60	CC	population ex vivo in a mammal (by allowing a tumour associated lipid to
QY	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120	CC	contact APCs, in which receptors for the tumour associated lipids are
Db	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120	CC	inactivated or deleted to produce a tumouricidally activated population,
QY	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174	CC	and administering APCs to the host), producing a tumouricidal T cell
Db	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174	CC	population ex vivo in a mammal) by allowing a tumour associated lipids to
RESULT 2		CC	contact T cells, in which adaptor proteins, which inhibit T cell
ABU79079		CC	activation by tumour associated antigens, are deleted or functionally
ID	ABU79079 standard; protein; 174 AA.	CC	deactivated to produce a tumouricidal population of T cells, and
AC	ABU79079;	CC	administering the tumouricidally activated T cells to the host, or
XX		CC	allowing a superantigen-lipid raft to contact T cells ex vivo, and
DT	18-JUN-2003 (first entry)	CC	administering the tumouricidally activated T cells to the host), treating
XX	N. meningitidis lipopolysaccharide protein.	CC	(M5) cancer in a mammal (by administering a lipid binding molecule which
XX		CC	binds immunosuppressive tumour associated lipids in vivo), producing (M6)
KN	Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;	CC	a tumouricidal T cell population in vivo in a mammal (by allowing a
KW	gene therapy; mammalian cell receptor; cytostatic;	CC	tumour associated antigen to contact immunocytes in which adaptor
KW	tumour associated lipid; anergy; T cell; antigen presenting cell; APC;	CC	proteins which inhibit T cell activation by tumour associated antigens
KW	tumouricidal immunocyte; antitumour.	CC	are deleted or functionally deactivated) and producing (M7) a
OS	Neisseria meningitidis.	CC	tumouricidal T cell population ex vivo in a mammal comprising allowing a
XX		CC	superantigen-lipid raft conjugate to contact immunocytes in vivo. The
PN	US2002177551-A1.	CC	receptors, methods and compositions are useful for treating cancers and
XX		CC	tumours. Bacterial superantigens are co-administered or administered as
PD	28-NOV-2002.	CC	fusion constructs with anti-tumour proteins or motifs. The present
XX		CC	sequence represents an anti-tumour protein which is co-administered with
PF	30-MAY-2001; 2001US-00870759.	CC	or incorporated into a fusion construct with a superantigen. Note: The
XX		CC	sequence data for this patent did not form part of the printed
XX		CC	specification, but was obtained in electronic format from the US patent
PR	31-MAY-2000; 2000US-0208128P.	CC	office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX	(TERM/) Terman D S.	XX	
PA	Terman DS;	SQ	Sequence 174 AA;
PI			Query Match 100.0%; Score 868; DB 6; Length 174;
XX			Best Local Similarity 100.0%; Pred. No. 9.3e-87;
XX			Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX		QY	1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
XX		Db	1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGAKGSPRISAGYRINDLR 60
DR	WPI; 2003-361759/34.	QY	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120
DR	N-PSDB; ACA64711.	Db	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGSDSF 120
XX		QY	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
PT	A mammalian cell receptor, useful in the treatment of cancer by binding	Db	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVVRKF 174
PT	to tumour associated lipids where the binding induces energy or apoptosis		
PT	in T cells and antigen presenting cells.		
XX			
PS	Disclosure; Page; 167pp; English.		
XX		RESULT 3	
CC	The invention relates to a mammalian cell receptor, useful in the	ADP43316	
CC	treatment of cancer, which binds to tumour associated lipids and induces	ID	ADP43316 standard; protein; 174 AA.
CC	energy or apoptosis in the T cells and antigen presenting cells (APCs).	XX	
CC	Also included are a mammalian cell useful in the treatment of cancer	AC	ADP43316;
CC	where the receptor which binds tumour associated lipids and induces	XX	
CC	cellular inactivation or death is deleted or functionally deactivated,	DT	12-FEB-2004 (first entry)
CC	producing (M1) a tumouricidal immunocyte population in vivo in a mammal	XX	
CC	(by allowing tumour associated lipids to contact immunocytes in which	DE	N. meningitidis lipopolysaccharide seq id 36.
CC	receptors for immunosuppressive fatty acids, ceramides, glycolipids,	XX	
CC	sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,	KW	receptor; lipid-based tumour associated antigen; cytostatic;
		KW	antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
		KW	infectious disease; lipopolysaccharide; LPS.



OS Neisseria meningitidis.  
 PN US2003157113-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 28-DEC-2000; 2000US-00751708.  
 XX  
 PR 28-DEC-1999; 99US-0173371P.  
 XX  
 PA (TERM/) Terman D S.  
 XX  
 PI Terman DS;  
 XX  
 DR WPI; 2003-787326/74.  
 DR N-PSDB; ADF43315.  
 XX  
 PT New receptor in a mammalian cell that inhibits regular activation by  
 PT receptors specific for lipid-based tumor associated antigens, useful for  
 PT treating a neoplastic disease or tumor, and infectious diseases.  
 XX  
 PS Disclosure; SEQ ID NO 36; 151pp; English.  
 XX  
 CC The invention describes a receptor in a mammalian cell that inhibits  
 CC regular activation by receptors specific for lipid-based tumor  
 CC associated antigen. The receptor has cytostatic and antimicrobial  
 CC properties and is suitable for use in gene therapy. The receptors,  
 CC methods and compositions are useful for treating a neoplastic disease or  
 CC tumor (cancer), and infectious diseases. This is the amino acid sequence  
 CC of Neisseria meningitidis lipopolysaccharide (LPS) to which tumor cells  
 CC develop immunity.  
 XX  
 SQ Sequence 174 AA;  
 Query Match 100.0%; Score 868; DB 7; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-87;  
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNARSVDLGGSDSF 120  
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNARSVDLGGSDSF 120  
 QY 121 SQTSLGLGLVTCGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVRVKF 174  
 DB 121 SQTSLGLGLVTCGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVRVKF 174  
 RESULT 4  
 ADL16114  
 ID ADL16114 standard; protein; 174 AA.  
 AC ADL16114;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Neisseria meningitidis NspA for use in vaccine.  
 XX  
 KW Outer membrane vesicle preparation; OMV; detergent-free;  
 KW physical disruption; vaccine; serogroup B; NspA;  
 KW Neisserial surface protein A; immunogen.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN WO2004019977-A2.  
 XX  
 PD 11-MAR-2004.  
 XX  
 PF 01-SEP-2003; 2003WO-IB004293.  
 XX

PR 30-AUG-2002; 2002GB-00020194.  
 XX  
 PA (CHIR ) CHIRON SRL.  
 XX  
 PI Pizza M, Serruto D, Rappuoli R;  
 XX  
 DR WPI; 2004-239124/22.  
 XX  
 PT Producing an outer membrane vesicle (OMV) preparation from a bacterium,  
 PT useful as a vaccine against Neisseria meningitidis serogroup B, comprises  
 PT disrupting the bacterial membrane in the absence of deoxycholate  
 PT detergent.  
 XX  
 PS Disclosure; Fig 3; 20pp; English.  
 XX  
 CC The invention relates to a process for producing an outer membrane  
 CC vesicle (OMV) preparation from a bacterium. The process involves  
 CC disrupting the bacterial membrane substantially in the absence of  
 CC deoxycholate detergent or other detergent, followed by several  
 CC centrifugation steps. Membrane disruption is achieved by sonication,  
 CC homogenisation, microfluidisation, cavitation, osmotic shock, grinding,  
 CC French press, belnding or any other physical technique. The outer  
 CC membrane vesicles can be prepared from bacteria of the genera Moraxella,  
 CC Shigella, Pseudomonas, Treponema, Porphyromonas, Helicobacter or  
 CC Neisseria, and are particularly produced from Neisseria meningitidis  
 CC (especially serogroup B) or Neisseria gonorrhoeae. The invention also  
 CC relates to a Neisseria meningitidis outer membrane vesicle composition in  
 CC which the vesicles include the immunogens NspA (Neisserial surface  
 CC protein A; ADL16114), 287 protein (ADL16113) and 741 protein (ADL16112);  
 CC and the use of outer membrane vesicle compositions as a medicament,  
 CC especially for raising an immune response in a patient. The method is  
 CC useful for manufacturing an outer membrane vesicle preparation as a  
 CC vaccine against Neisseria meningitidis serogroup B. The present sequence  
 CC represents Neisseria meningitidis NspA.  
 XX  
 SQ Sequence 174 AA;  
 Query Match 100.0%; Score 868; DB 8; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-87;  
 Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNARSVDLGGSDSF 120  
 DB 61 FAVDYTRYKNYKAPSTDPKLYSIGASAIYDFTQSPVKPYLGARLSLNARSVDLGGSDSF 120  
 QY 121 SQTSLGLGLVTCGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVRVKF 174  
 DB 121 SQTSLGLGLVTCGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSVGVRVKF 174  
 RESULT 5  
 ADL13428  
 ID ADL13428 standard; protein; 174 AA.  
 XX  
 AC ADL13428;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Neisseria meningitidis H44/76 full-length NspA protein.  
 XX  
 KW Neisserial surface protein A; NspA; refolding; recombinant production;  
 KW vaccine; subunit vaccine; prevention; diagnosis; meningococcus;  
 KW invasive bacterial disease; bacteraemia; meningitis;  
 KW Neisseria gonorrhoeae; gonorrhoea; mature protein; strain H44/76;  
 KW antibacterial; gene therapy.  
 XX  
 OS Neisseria meningitidis; H44/76.  
 XX  
 PF Key Location/Qualifiers  
 XX



RESULT 9  
AAW04893

ID	AAW04893 standard; protein; 174 AA.	ID	AAW04894 standard; protein; 174 AA.
XX	AAW04893;	XX	AAW04894;
AC		AC	
XX		XX	
DT	16-OCT-2003 (revised)	DT	16-OCT-2003 (revised)
DT	22-DEC-1996 (first entry)	DT	22-DEC-1996 (first entry)
XX		XX	
DE	Proteinase K resistant N. meningitidis 22 kD surface protein.	DE	Proteinase K resistant N. meningitidis 22 kD surface protein.
XX		XX	
KW	Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;	KW	Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;
KW	antibody; detection; probe; surface protein.	KW	antibody; detection; probe; surface protein.
XX		XX	
OS	Neisseria meningitidis; strain Z4063.	OS	Neisseria meningitidis; strain b2.
XX		XX	
FH	Key Location/Qualifiers	FH	Key Location/Qualifiers
FT	Peptide 1..19	FT	Peptide 1..19
FT	/label= sig_peptide	FT	/label= sig_peptide
FT	Protein 20..174	FT	Protein 20..174
FT	/label= mat_protein	FT	/label= mat_protein
XX		XX	
PN	WO9629412-A1.	PN	WO9629412-A1.
XX		XX	
PD	26-SEP-1996.	PD	26-SEP-1996.
XX		XX	
PF	15-MAR-1996; 96WO-CA000157.	PF	15-MAR-1996; 96WO-CA000157.
XX		XX	
PR	17-MAR-1995; 95US-00406362.	PR	17-MAR-1995; 95US-00406362.
PR	04-AUG-1995; 95US-0001983P.	PR	04-AUG-1995; 95US-0001983P.
XX		XX	
PA	(IAPB-) IAF BIO VAC INC.	PA	(IAPB-) IAF BIO VAC INC.
XX		XX	
PI	Brodeur BR, Martin D, Hamel J, Rioux C;	PI	Brodeur BR, Martin D, Hamel J, Rioux C;
XX		XX	
DR	WPI: 1996-443187/44.	DR	WPI: 1996-443187/44.
DR	N-PSDB; AAT39041.	DR	N-PSDB; AAT39042.
XX		XX	
PT	Neisseria meningitidis antigen, highly conserved between different	PT	Neisseria meningitidis antigen, highly conserved between different
PT	strains - useful for prodn. of antibodies for immunisation against, or	PT	strains - useful for prodn. of antibodies for immunisation against, or
PT	diagnosis of, N. meningitidis infection.	PT	diagnosis of, N. meningitidis infection.
XX		XX	
PS	Claim 7; Fig 9; 117pp; English.	PS	Claim 7; Fig 10; 117pp; English.
XX		XX	
CC	A proteinase K resistant surface protein has been isolated from 4 strains	CC	A proteinase K resistant surface protein has been isolated from 4 strains
CC	of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,	CC	of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,
CC	antigenic fragments of antibodies can be used in a vaccine for the	CC	antigenic fragments of antibodies can be used in a vaccine for the
CC	prevention of infection by N. meningitidis or by N. gonorrhoeae in	CC	prevention of infection by N. meningitidis or by N. gonorrhoeae in
CC	humans. The antibodies may also be used diagnostically to detect N.	CC	humans. The antibodies may also be used diagnostically to detect N.
CC	meningitidis infection. The antigen may also be used to detect antibodies	CC	meningitidis infection. The antigen may also be used to detect antibodies
CC	specific to N. meningitidis antigen. DNA sequences encoding the antigen,	CC	specific to N. meningitidis antigen. DNA sequences encoding the antigen,
CC	or their fragments, can be used as probes for the detection of pathogenic	CC	or their fragments, can be used as probes for the detection of pathogenic
CC	Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)	CC	Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
XX		XX	
SQ	Sequence 174 AA;	SQ	Sequence 174 AA;
Query Match 98.4%; Score 854; DB 2; Length 174;		Query Match 95.0%; Score 825; DB 2; Length 174;	
Best Local Similarity 98.3%; Pred. No. 3.2e-85;		Best Local Similarity 94.3%; Pred. No. 4.8e-82;	
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;	
QY	1 MKKALATLIALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60	QY	1 MKKALATLIALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db	1 MKKALATLIALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60	Db	1 MKKALATLIALPAALAEAGSGFVQDAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
QY	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120	QY	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
Db	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120	Db	61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
QY	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174	QY	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
Db	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174	Db	121 SQTSLGLVLTGVSVAVTNPVLDAGYRNYIGKNTVKNVRSGLSVGVKVF 174
RESULT 10		RESULT 11	
AAW04894		ABG91063	

ID ABG91063 standard; protein; 174 AA.  
 AC ABG91063;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Neisseria gonorrhoeae outer membrane protein #1.  
 XX  
 KW Gran-negative bacterial bleb; PorB; outer membrane protein;  
 KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;  
 KW protective antigen; antibacterial; vaccine.  
 XX  
 OS Neisseria gonorrhoeae.  
 XX  
 PN WO200262380-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 08-FEB-2002; 2002WO-EP001356.  
 XX  
 PR 08-FEB-2001; 2001GB-00003169.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;  
 XX  
 DR WPI; 2002-657510/70.  
 DR N-PSDB; ABS67381.  
 XX  
 XX Novel gran-negative bacterial bleb presenting on its surface PorB outer  
 PT membrane protein from Chlamydia trachomatis or protective antigen from  
 PT Chlamydia pneumoniae; useful for preventing Chlamydia infection.  
 XX  
 PS Disclosure; Page 54; 75pp; English.  
 XX  
 CC The present invention relates to a new gram-negative bacterial bleb  
 CC presenting on its surface the PorB outer membrane protein from Chlamydia  
 CC trachomatis, or a protective antigen from C. pneumoniae. The invention is  
 CC useful for preventing C. trachomatis or C. pneumoniae infection in a  
 CC host. The present amino acid sequence represents a Neisseria gonorrhoeae  
 CC protein as described in the invention  
 XX  
 SQ Sequence 174 AA;  
 Query Match 95.0%; Score 825; DB 5; Length 174;  
 Best Local Similarity 94.3%; Pred. No. 4.8e-82;  
 Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALAALIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDSF 120  
 DB 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYFGARLSLNRSASVLDGSDSF 120  
 QY 121 SOTSIGLGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGBLSVGVRVKF 174  
 DB 121 SKTSAGLGLVLAGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGBLSAGVRVKF 174  
 RESULT 12  
 ID AAW04892 standard; protein; 175 AA.  
 XX  
 AC AAW04892;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 22-DEC-1996 (first entry)  
 XX  
 DE Proteinase K resistant N. meningitidis 22 kD surface protein.  
 XX  
 KW Proteinase K resistant; Neisseria meningitidis; Neisseria gonorrhoeae;

KW antibody; detection; probe; surface protein.  
 XX  
 OS Neisseria meningitidis; strain MCH88.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT Protein /label= sig\_peptide  
 FT 20..175  
 FT /label= mat\_protein  
 PN WO9629412-A1.  
 XX  
 PD 26-SEP-1996.  
 XX  
 PF 15-MAR-1996; 96WO-CA000157.  
 XX  
 PR 17-MAR-1995; 95US-00406362.  
 PR 04-AUG-1995; 95US-0001983P.  
 XX  
 PA (IAFB-) IAF BIO VAC INC.  
 XX  
 PI Brodeur BR, Martin D, Hamel J, Rioux C;  
 XX  
 DR WPI; 1996-443187/44.  
 DR N-PSDB; AAT39040.  
 XX  
 XX Neisseria meningitidis antigen, highly conserved between different  
 PT strains - useful for prodn. of antibodies for immunisation against, or  
 PT diagnosis of, N. meningitidis infection.  
 XX  
 PS Claim 7; Fig 8; 117pp; English.  
 CC  
 CC A proteinase K resistant surface protein has been isolated from 4 strains  
 CC of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen,  
 CC antigenic fragments of antibodies can be used in a vaccine for the  
 CC prevention of infection by N. meningitidis or by N. gonorrhoeae in  
 CC humans. The antibodies may also be used diagnostically to detect N.  
 CC meningitidis infection. The antigen may also be used to detect antibodies  
 CC specific to N. meningitidis antigen. DNA sequences encoding the antigen,  
 CC or their fragments, can be used as probes for the detection of pathogenic  
 CC Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 175 AA;  
 Query Match 95.0%; Score 824.5; DB 2; Length 175;  
 Best Local Similarity 95.4%; Pred. No. 5.5e-82;  
 Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALAALIALALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVLDGSDS 119  
 DB 61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDFNGSDS 120  
 QY 120 FSQTSIGLGLVLTGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGBLSVGVRVKF 174  
 DB 121 FSQTSIGLGLVLAGVSAYVTPNVDLDAGYRNYIGKNTVKNVRSGBLSAGVRVKF 175  
 RESULT 13  
 ID ADL24385 standard; protein; 166 AA.  
 XX  
 AC ADL24385;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE N meningitidis strain 608B modified NspA protein #3.  
 XX  
 KW mutein; mutant; NspA; vaccine; antibacterial; meningitis.  
 XX

OS Neisseria meningitidis.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 35..36  
 FT /note= "wild-type NspA residues 36-43 deleted"  
 XX  
 PN WO2004019976-A2.  
 XX  
 PD 11-MAR-2004.  
 XX  
 PF 29-AUG-2003; 2003WO-CA001452.  
 XX  
 PR 30-AUG-2002; 2002US-0406980P.  
 XX  
 PA (SHIR-) SHIRE BIOCHEM INC.  
 XX  
 PI Martin D, Rioux S;  
 DR WPI; 2004-239123/22.  
 XX  
 XX Composition comprising liposome associated with isolated polypeptide or  
 PT polynucleotide derived from Neisseria meningitidis strain 608B, or its  
 PT fragment or analog, useful for inducing an immune response against N.  
 PT meningitidis.  
 PS  
 PS Example 4; Page; 79pp; English.  
 XX  
 CC The present invention relates to a pharmaceutical composition comprising  
 CC a liposome associated with an isolated polypeptide derived from Neisseria  
 CC meningitidis strain 608B, where the polypeptide is the NspA protein. The  
 CC composition is useful for inducing an immune response against N.  
 CC meningitidis, for preventing and/or treating N. meningitidis infection  
 CC and for treating and/or preventing neisserial infection chosen from N.  
 CC meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is  
 CC useful for treatment or prophylaxis of meningitis and meningococcal, in  
 CC a host. The host is a mammal, preferably a human and more preferably an  
 CC adult human. The present sequence is a modified version of the Neisseria  
 CC meningitidis strain 608B NspA protein. Note: This sequence is not shown  
 CC in the specification but has been created based on the information given  
 CC and the wild-type NspA protein shown in Figure 1.  
 XX  
 XX Sequence 166 AA;  
 SQ  
 Query Match 94.5%; Score 820; DB 8; Length 166;  
 Best Local Similarity 95.4%; Pred. No. 1.6e-81;  
 Matches 166; Conservative 0; Mismatches 0; Indels 8; Gaps 1;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAK-----KGFSPRISAGYRINDLR 52  
 QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 120  
 DB 53 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDSF 112  
 QY 121 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYNYIGKVTNKNVRSGLSVGVVRVKF 174  
 DB 113 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYNYIGKVTNKNVRSGLSVGVVRVKF 166  
 RESULT 14  
 ABP77991  
 ID ABP77991 standard; protein; 175 AA.  
 XX  
 AC ABP77991;  
 XX  
 XX 07-MAR-2003 (first entry)  
 DT  
 DE N. gonorrhoeae amino acid sequence SEQ ID 2512.  
 XX  
 KW Antibacterial; infection; vaccine; gene therapy.  
 XX

OS Neisseria gonorrhoeae.  
 XX  
 PN WO200279243-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 12-FEB-2002; 2002WO-IB002069.  
 XX  
 PR 12-FEB-2001; 2001GB-00003424.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 XX  
 PI Fontana MR, Pizza M, Massignani V, Monaci E;  
 DR WPI; 2003-058415/05.  
 DR N-PSDB; AB238961.  
 XX  
 PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
 PT medicament for treating or preventing N. gonorrhoeae infection.  
 XX  
 PS Disclosure; Page 371; 815pp; English.  
 XX  
 CC The present invention relates to proteins from Neisseria gonorrhoeae.  
 CC Also disclosed are the nucleic acid molecules encoding the proteins and  
 CC antibodies that specifically bind to the proteins. The composition  
 CC comprising the protein, nucleic acid or antibody is useful for the  
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
 CC infection, this may be in the form of a vaccine or gene therapy.  
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid  
 CC molecules of the invention  
 XX  
 SQ Sequence 175 AA;  
 Query Match 93.3%; Score 809.5; DB 6; Length 175;  
 Best Local Similarity 93.1%; Pred. No. 2.5e-80;  
 Matches 163; Conservative 2; Mismatches 9; Indels 1; Gaps 1;  
 QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60  
 QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 119  
 DB 61 FAVDYTRYKNYKQAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSASVDLGGSDS 120  
 QY 120 SQTSGIGLVLTGVSAYVTPNVLDAGYRNYNYIGKVTNKNVRSGLSVGVVRVKF 174  
 DB 121 FSKTSAGLVLAGVSAYVTPNVLDAGYRNYNYIGKVTNKNVRSGLSVGVVRVKF 175  
 RESULT 15  
 ADL24387  
 ID ADL24387 standard; protein; 162 AA.  
 XX  
 AC ADL24387;  
 XX  
 XX 03-JUN-2004 (first entry)  
 DT  
 XX N meningitidis strain 608B modified NspA protein #5.  
 DE  
 XX mutein; mutant; NspA; vaccine; antibacterial; meningitis.  
 KW  
 XX Neisseria meningitidis.  
 OS  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 151..152  
 FT /note= "wild-type NspA residues 152-163 deleted"  
 XX  
 PN WO2004019976-A2.  
 XX  
 PD 11-MAR-2004.  
 XX

```

PF 29-AUG-2003; 2003WO-CA001452.
XX
PR 30-AUG-2002; 2002US-0406980P.
XX
PA (SHIR-) SHIRE BIOCHEM INC.
XX
PI Martin D, Rioux S;
XX
DR WPI; 2004-239123/22.
XX
XX Composition comprising liposome associated with isolated polypeptide or
PT polynucleotide derived from Neisseria meningitidis strain 608B, or its
PT fragment or analog, useful for inducing an immune response against N.
PT meningitidis.
XX
XX
PS Example 4; Page; 79pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
CC a liposome associated with an isolated polypeptide derived from Neisseria
CC meningitidis strain 608B, where the polypeptide is the NpA protein. The
CC composition is useful for inducing an immune response against N.
CC meningitidis, for preventing and/or treating N. meningitidis infection
CC and for treating and/or preventing neisserial infection chosen from N.
CC meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharaea. It is
CC useful for treatment or prophylaxis of meningitis and meningococemia, in
CC a host. The host is a mammal, preferably a human and more preferably an
CC adult human. The present sequence is a modified version of the Neisseria
CC meningitidis strain 608B NpA protein. Note: This sequence is not shown
CC in the specification but has been created based on the information given
CC and the wild-type NpA protein shown in Figure 1.
XX
SQ Sequence 162 AA;

      Query Match      91.5%; Score 794; DB 8; Length 162;
      Best Local Similarity 93.1%; Pred No. 1,1e-78;
      Matches 162; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
   |||||
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDEPTQSPVKPYLGARLSINRASVDLGGSDSF 120
   |||||
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDEPTQSPVKPYLGARLSINRASVDLGGSDSF 120

Qy 121 SQTSLGLGLVLTGVSVAVTPNVLDAGYRNYIGKNTVKNRSGELSVGVRVKF 174
   |||||
Db 121 SQTSLGLGLVLTGVSVAVTPNVLDAGYRNY-----GELSVGVRVKF 162

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Search completed: May 19, 2005, 20:55:00  
 Job time : 304 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 19, 2005, 20:41:43 ; Search time 113 Seconds  
(without alignments)  
114.946 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868  
Sequence: 1 MKKALATLIALPAALAE.....VNTKVRNSGELSGVGRVKF 174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	174	3	US-08-913-362-2
2	854	98.4	174	3	US-08-913-362-6
3	838.5	96.6	175	3	US-08-913-362-30
4	825	95.0	174	3	US-08-913-362-8
5	824.5	95.0	175	3	US-08-913-362-4
6	135	15.6	170	1	US-08-127-499A-20
7	135	15.6	170	1	US-08-482-847-20
8	133	15.3	25	3	US-08-913-362-26
9	113.5	13.1	98	4	US-09-540-236-2245
10	109.5	12.6	187	4	US-09-489-039A-13699
11	104.5	12.0	384	4	US-09-543-681A-7922
12	93	10.7	190	4	US-09-543-681A-7684
13	92.5	10.7	261	4	US-09-252-991A-19759
14	89.5	10.3	186	4	US-09-540-236-2792
15	89.5	10.3	385	4	US-09-489-039A-7451
16	88.5	10.2	180	4	US-09-164-714-7
17	88.5	10.2	573	3	US-09-336-447A-3
18	88.5	10.2	573	4	US-09-952-267B-3
19	88	10.1	359	1	US-08-457-997B-2
20	88	10.1	359	3	US-08-467-722A-2
21	88	10.1	359	4	US-09-451-184-2
22	88	10.1	397	4	US-09-902-540-16267
23	88	10.1	610	3	US-09-336-447A-11
24	88	10.1	610	4	US-09-952-267B-11
25	88	10.1	624	3	US-09-336-447A-7
26	88	10.1	624	4	US-09-952-267B-7
27	88	10.1	889	3	US-09-336-447A-15

28	88	10.1	889	4	US-09-952-267B-15	Sequence 15, Appl
29	87.5	10.0	708	4	US-09-336-115C-2	Sequence 2, Appl
30	87	10.0	16	3	US-08-913-362-15	Sequence 15, Appl
31	87	10.0	500	4	US-09-325-932A-149	Sequence 149, Appl
32	86	9.9	512	4	US-09-059-584-57	Sequence 57, Appl
33	85.5	9.9	238	4	US-09-902-540-12284	Sequence 12284, A
34	85.5	9.9	487	4	US-09-328-352-5331	Sequence 5331, Ap
35	85	9.8	568	5	PCT-US95-13749-5	Sequence 5, Appl
36	84.5	9.7	643	4	US-09-328-352-5146	Sequence 5146, Ap
37	84	9.7	351	4	US-09-252-991A-30094	Sequence 30094, A
38	83.5	9.6	721	4	US-09-328-352-7781	Sequence 7781, Ap
39	83	9.6	364	4	US-09-418-980-8	Sequence 8, Appl
40	83	9.6	364	4	US-09-809-665A-151	Sequence 151, Appl
41	82	9.4	172	4	US-09-902-540-14682	Sequence 14682, A
42	82	9.4	433	2	US-08-883-515-2	Sequence 2, Appl
43	82	9.4	512	4	US-09-059-584-56	Sequence 56, Appl
44	82	9.4	867	4	US-09-540-236-2676	Sequence 2676, Ap
45	81	9.3	15	3	US-08-913-362-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-08-913-362-2  
; Sequence 2, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 04/9998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-913-362-2

Query Match 100.0%; Score 868; DB 3; Length 174;

Best Local Similarity 100.0%; Pred. No. 7.9e-93;  
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60  
Db 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKXKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120  
Db 61 FAVDYTRYKXKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120

QY 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174  
Db 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174

QY 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174  
Db 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 2

US-08-913-362-6  
; Sequence 6, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-913-362-6

Query Match 98.4%; Score 854; DB 3; Length 174;  
Best Local Similarity 98.3%; Pred. No. 3.4e-91;  
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60  
Db 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKXKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120  
Db 61 FAVDYTRYKXKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDSF 120

QY 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174  
Db 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174

RESULT 3

US-08-913-362-30  
; Sequence 30, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-913-362-30

Query Match 96.6%; Score 838.5; DB 3; Length 175;  
Best Local Similarity 97.1%; Pred. No. 2.2e-89;  
Matches 170; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60  
Db 1 MKKALATLIALPAAALAEAGSGFVQADAAHAKASSILGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKXKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDS 119  
Db 61 FAVDYTRYKXKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRSVDLGGSDS 120

QY 120 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174  
Db 120 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKNTVKNVRSGLSVGVVKF 174

Db 121 FSQTSXGLGLAGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

RESULT 4

US-08-913-362-8  
; Sequence 8, Application US/08913362  
; Patent No. 6287574

; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,362  
; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-913-362-8  
Query Match 95.0%; Score 825; DB 3; Length 174;  
Best Local Similarity 94.3%; Pred. No. 7.9e-88;  
Matches 164; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALAALIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYFGARLSLNRAVAHLLGGSDSF 120

QY 121 SOTSIGLGLTGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 SKTSAGLGLAGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

RESULT 5

US-08-913-362-4  
; Sequence 4, Application US/08913362  
; Patent No. 6287574

; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,362  
; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-913-362-4  
Query Match 95.0%; Score 824.5; DB 3; Length 175;  
Best Local Similarity 95.4%; Pred. No. 9.1e-88;  
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

Db 1 MKKALAALIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDS 119

Db 61 FAVDYTRYKNYKQVPESTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDS 120

QY 120 FSQTSIGLGLTGVSYAVTPNVLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 174

Db 121 FSQTSIGLGLAGVSAYATPNVDLDAGYRNYIGKNTVKNVRSGLSAGVRVKF 175

RESULT 6.

US-08-127-499A-20  
; Sequence 20, Application US/08127499A  
; Patent No. 5510264  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:

```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-482-847-20

Query Match 15.6%; Score 135, DB 1; Length 170;
Best Local Similarity 26.3%; Pred. No. 1.3e-07;
Matches 41; Conservative 20; Mismatches 47; Indels 48; Gaps 4;

QY 6 ATLLALPALAALGASGFYVQADAAH-----AKASSSLGS-----AKG 45
DB 15 SELLSSAAQAASERSFYVQADLAYAERITHDYPOATGANNTSTVSDYFRNIRAH 74
QY 46 FSPRISAGYRINDLRAPVDTRYKNY-----KAPSTDPK 79
DB 75 IHPRVSGVDFGWRIAADYASRYKWNKNKYSVNTKELENKHNKKDLKTENQENGTFFHA 134
QY 80 LYSIGASAIYDFTQSPVKPYLGARLSLN--RASVD 113
DB 135 ASSLGLSAIYDFKLKGKPKPYGARVAYGHVRHSID 170

RESULT 8
US-08-913-362-26
; Sequence 26, Application US/08913362
; Patent No. 6287574
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768

```

REFERENCE/DOCKET NUMBER: 047998/0128  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO. 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Neisseria meningitidis  
STRAIN: 608B  
US-08-913-362-26

Query Match 15.3%; Score 133; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGA 85  
DB 1 FAVDYTRYKNYKAPSTDFKLYSIGA 25

RESULT 9

US-09-540-236-2245  
Sequence 2245, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2005-001  
CURRENT APPLICATION NUMBER: US/09/540,236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 2245  
LENGTH: 98  
TYPE: PRT  
ORGANISM: M. catarrhalis  
US-09-540-236-2245

Query Match 13.1%; Score 113.5; DB 4; Length 98;  
Best Local Similarity 37.9%; Pred. No. 1.8e-05;  
Matches 22; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

QY 122 QTSIGLGLTGVSYAVTPNVDLDAGRYNYIG---KVTYKVRSGE--LSGVVRVKF 174  
DB 41 ETKVGFVLAGAQAYNQLSDAGVEYNLYGKYDKLDLTASKAKAHQYGAQVGLRHF 98

RESULT 10

US-09-489-039A-13699  
Sequence 13699, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 13699  
LENGTH: 187  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13699

Query Match 12.6%; Score 109.5; DB 4; Length 187;

Best Local Similarity 25.2%; Pred. No. 0.00014;  
Matches 51; Conservative 26; Mismatches 78; Indels 47; Gaps 7;  
QY 1 MKKALATLIA--LALPAAALAEAGSGFYVQVQADAAHAKASSLSGSAK-----44  
DB 5 MKSIAAKKVAVTIALGASSAACAAVNLHGEAGFTNLASFGAGEPGMTFTSSQWAHSDN 64  
QY 45 -GFSPRISAGYRINDLRPAVDYTRYKNYKAPSTDFKLYSIGASAIY----DFDTQSPVKP 99  
DB 65 DGDVGLGMGYNFGNLPF-----LMTLGKAVYLNPKDDEGYATAA 106  
QY 100 YLGARLSINRASVDLGGSDSFSQTSIGLGV-----LTGVSVAVTNPVLDLADAGVY-NYI 152  
DB 107 GGAELPLGQ-YFTLFGEGYYSPDSMSSGVDEYVANNAGVRLNVRPSLNIEAGYRIIDMA 165  
QY 153 GKVTYKVRSGELSGVVRVKF 174  
DB 166 GKDGNRNTLADGAYAGVNFVF 187

RESULT 11

US-09-543-681A-7922  
Sequence 7922, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 7922  
LENGTH: 384  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-7922

Query Match 12.0%; Score 104.5; DB 4; Length 384;  
Best Local Similarity 26.1%; Pred. No. 0.0016;  
Matches 55; Conservative 27; Mismatches 86; Indels 43; Gaps 13;

QY 1 MKKALATLIAALPAAALAEAGSG-----FYVQADAAHAKASS-----SLGSARKGF 46  
DB 23 MKK---TAIALAVAAAFATAQAAPKDNWTYTGKLGWSQYQSTGNWWDGWNIGNGSTH 79  
QY 47 SPRIS---AGYRIND---LRFVDYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97  
DB 80 KDQICAGAFAGYQYNQVGLGFELGYDWLGRMAYKGSYNNGAFAKQGIQLTTKLSYPMDDL 139  
QY 98 KPY--LGARL-----SLNRASVDLGGSDSFSQTSIGLGLV--TGVSVAVTNPVLDLADAG 146  
DB 140 DVTYTLGGVMWRADSTATINATSA--GTQKRFSENDCGVPFALGTGTAITPNIATRL 197  
QY 147 YRY-NYIGKVTYKVR--SGELSGVVRVKF 174  
DB 198 YQWNNIGDKGTL-NARPDNGMLSVGVAYRF 227

RESULT 12

US-09-543-681A-7684  
Sequence 7684, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706



Search completed: May 19, 2005, 21:04:18  
Job time : 113 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 19, 2005, 20:34:09 ; Search time 69 Seconds  
(without alignments)  
242.634 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868  
Sequence: 1 MKKALATLIALPAALAE.....VNTVKNVRSBELSVGVKVF 174

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	864	99.5	174	2 G81174	outer membrane pro
2	854	98.4	174	2 B81932	outer membrane pro
3	244.5	28.2	261	2 S16610	opacity protein op
4	242	27.9	260	2 S16611	opacity protein op
5	241.5	27.8	338	2 S16613	opacity protein op
6	241	27.8	258	2 S16612	opacity protein op
7	241	27.8	260	1 KONHO	opacity protein op
8	240.5	27.7	237	2 S36343	opacity protein op
9	240.5	27.7	257	2 S16614	opacity protein op
10	239	27.5	266	2 S16616	opacity protein op
11	238	27.4	258	2 S08514	opacity protein-re
12	237	27.3	254	2 S20043	opacity protein B
13	237	27.3	270	2 S04380	opacity protein P.
14	236.5	27.2	268	1 KONH2C	opacity protein P.
15	236	27.2	283	2 S72343	opacity protein op
16	232.5	26.8	234	2 S36329	opacity protein op
17	232.5	26.8	282	2 S16617	opacity protein op
18	232	26.7	234	2 S36342	opacity protein op
19	232	26.7	234	2 S36341	opacity protein op
20	231	26.6	233	2 S36350	opacity protein op
21	226	26.0	234	1 KONH8	opacity protein V2
22	226	26.0	234	2 S36348	opacity protein op
23	226	26.0	238	2 S36349	opacity protein op
24	226	26.0	261	2 S16619	opacity protein op
25	224.5	25.9	243	2 S36346	opacity protein op
26	221	25.5	248	2 PL0038	opacity protein D.
27	219	25.2	238	2 S36344	opacity protein op
28	217	25.0	178	2 F64124	opacity protein ho
29	215	24.8	239	2 S28630	opacity protein op

RESULT 1

G81174

outer membrane protein Nega NMB0663 [imported] - Neisseria meningitidis (strain MC58 sero

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: G81174

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; PMID:2017555; PMID:10710307

A:Accession: G81174

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <TET>

A:Cross-references: UNIPROT:Q9RP17; GB:AE002420; GB:AE002098; NID:g7225876; PIDN:AAF41081

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0663

Query Match 99.5%; Score 864; DB 2; Length 174;

Best Local Similarity 99.4%; Pred. No. 1.4e-69;

Matches 173; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

DB 1 MKKALATLIALPAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFPKLYSIGASALYDPTQSPVKPYLGARLSLNARSLDGGSDSF 120

DB 61 FAVDYTRYKNYKAPSTDFPKLYSIGASALYDPTQSPVKPYLGARLSLNARSLDGGSDSF 120

QY 121 SQTSLGLGLVTCVSVYATPNVDLDAGYRNYIKVNTVKNVRSBELSVGVKVF 174

DB 121 SQTSLGLGLVTCVSVYATPNVDLDAGYRNYIKVNTVKNVRSBELSVGVKVF 174

RESULT 2

B81932

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain Z2491 serogro

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004

C:Accession: B81932

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagsals, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; PMID:20222556; PMID:10761919

A:Accession: B81932

A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-174 <PAR>  
A:Cross-references: UNIPROT:P95372; GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB8414  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: nspA; NMA0862

Query Match 98.4%; Score 854; DB 2; Length 174;  
Best Local Similarity 98.3%; Pred. No. 1.1e-68;  
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLALPAAALAEAGSGFFVQADAAHAKASSLSGSAKGSPRISAGYRINDLR 60  
Db 1 MKKALATLALPAAALAEAGSGFFVQADAAHAKASSLSGSAKGSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSGASAIYDFDTQSPVKPYLGARLSNRSVDLGGSDSF 120  
Db 61 FAVDYTRYKNYKAPSTDFKLYSGASAIYDFDTQSPVKPYLGARLSNRSVDLGGSDSF 120

QY 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKVTNKNRSGELSGVGRVKF 174  
Db 121 SQTSLGLVLTGVSAYATPNVDLDAGRYNYIGKVTNKNRSGELSGVGRVKF 174

RESULT 3  
Sl6610  
opacity protein opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)  
N:Alternate names: outer membrane protein opak  
C:Species: Neisseria gonorrhoeae  
A:Variety: strain MS11  
C:Date: 13-Jan-1995 #sequence\_revision 17-Oct-1997 #text\_change 17-Oct-1997  
C:Accession: Sl6610  
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991  
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein  
A:Reference number: Sl6610; MUID:92114767; PMID:1815562  
A:Accession: Sl6610  
A:Molecule type: DNA  
A:Residues: 1-261 <BHA>  
A:Cross-references: EMBL:X52364  
A:Experimental source: strain MS11, variant 4.8  
A:Note: the authors did not translate the sequence for the signal peptide  
A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein  
C:Genetics:  
A:Gene: opak  
C:Superfamily: opacity protein  
C:Keywords: cell surface component; transmembrane protein  
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
F:24-261/Product: opacity protein opak #status predicted <MAT>  
F:34-42/Domain: transmembrane #status predicted <TM1>  
F:43-75/Domain: extracellular #status predicted <EXT1>  
F:51-61/Region: semivariable region  
F:76-84/Domain: transmembrane #status predicted <TM2>  
F:89-95/Domain: transmembrane #status predicted <TM3>  
F:102-129/Region: hypervariable region HV1  
F:135-149/Domain: transmembrane #status predicted <TM4>  
F:155-165/Domain: transmembrane #status predicted <TM5>  
F:166-212/Domain: extracellular #status predicted <EXT3>  
F:171-218/Region: hypervariable region HV2  
F:213-225/Domain: transmembrane #status predicted <TM6>  
F:229-237/Domain: transmembrane #status predicted <TM7>  
F:238-252/Domain: extracellular #status predicted <EXT4>  
F:253-261/Domain: transmembrane #status predicted <TM8>

Query Match 28.2%; Score 244.5; DB 2; Length 261;  
Best Local Similarity 29.9%; Pred. No. 2.3e-14;  
Matches 73; Conservative 26; Mismatches 58; Indels 87; Gaps 10;

QY 15 AAALAEAGSGFFVQADAAHAKA-----SSLSGSAK-----FSPRI 50  
Db 21 AQASGNGGFFVQADLAAERITHDPEPTGAKGTTISTVDFRNIRTHSHPRV 80

QY 51 SAGYRINDLRFAVDYTRYKNY-----KAPSTDFK-----LYS 82  
Db 81 SVGYDFGGWRIADYARYKWNKNYSVSIKELLRNKGNRNTDLKAENQNGCTFFHAVSS 140

QY 83 IGASAIYDFDTQSPVKPYLGARLSN--RASVD-----LGG----- 116  
Db 141 LGLSAVDYDFKLNDFKPYIGARVAYGHVHRHSDTKTKTTEVTILHGPCTTPTVYPKNT 200

QY 117 -----SDSFSQTSIGLVLTGVSAYATPNVDLDAGRYNYIGKVTNKNRSGELSGV 170  
Db 201 QNAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGRYHYHWRLENTR-FKTHEASLGV 257

QY 171 RVKF 174  
Db 258 RVRF 261

RESULT 4  
Sl6611  
opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments)  
N:Alternate names: outer membrane protein opa58  
C:Species: Neisseria gonorrhoeae  
A:Variety: strain MS11  
C:Date: 04-Jun-1997 #sequence\_revision 17-Oct-1997 #text\_change 09-Jul-2004  
C:Accession: Sl6611; S36345; S28624  
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, M.; Microbiol. 5, 1889-1901, 1991  
A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein  
A:Reference number: Sl6610; MUID:92114767; PMID:1815562  
A:Accession: Sl6611  
A:Molecule type: DNA  
A:Residues: 1-260 <BHA>  
A:Cross-references: UNIPROT:O04882; EMBL:X52371  
A:Experimental source: strain MS11, variant 4.8  
A:Note: the authors did not translate the sequence for the signal peptide  
A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein  
R:Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F. EMBO J. 12, 641-650, 1993  
A:Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms of Neisseria gonorrhoeae  
A:Reference number: S36328; MUID:93178439; PMID:8440254  
A:Accession: S36345  
A:Molecule type: DNA  
A:Residues: 24-260 <KUP>  
A:Cross-references: EMBL:Z18937; NID:G49333; PIDN:CAA79370.1; PID:G940799  
A:Experimental source: strain MS11, variant F3  
A:Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein  
C:Genetics:  
A:Gene: opaJ  
C:Superfamily: opacity protein  
C:Keywords: cell surface component; transmembrane protein  
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
F:24-260/Product: opacity protein opaJ #status predicted <MAT>  
F:34-42/Domain: transmembrane #status predicted <TM1>  
F:43-74/Domain: extracellular #status predicted <EXT1>  
F:51-60/Region: semivariable region  
F:75-83/Domain: transmembrane #status predicted <TM2>  
F:88-94/Domain: transmembrane #status predicted <TM3>  
F:95-133/Domain: extracellular #status predicted <EXT2>  
F:101-128/Region: hypervariable region HV1  
F:134-148/Domain: transmembrane #status predicted <TM4>  
F:154-164/Domain: transmembrane #status predicted <TM5>  
F:165-211/Domain: extracellular #status predicted <EXT3>  
F:170-217/Region: hypervariable region HV2  
F:212-224/Domain: transmembrane #status predicted <TM6>  
F:228-236/Domain: transmembrane #status predicted <TM7>  
F:237-251/Domain: extracellular #status predicted <EXT4>  
F:252-260/Domain: transmembrane #status predicted <TM8>

Query Match 27.9%; Score 242; DB 2; Length 260;  
Best Local Similarity 29.5%; Pred. No. 3.9e-14;

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Db      157 HPRVSVGDFGGWRIADYARYRKWNKNYSVDIKELNKNQKRDLTENQENGTFHAY 216
        ||:|||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Qy      81 YSICASAIYDPTDSPVKPYLGARLSLN--RASVD-----LGG----- 116
        :||::|||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Db      217 SSLGLSAVIDFKLNDKFPIGARVAVGHVRSIDSTKTKTFLTSYSGGLNPVTVVTEEN 276
        :||::|||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Qy      117 -----SDSFQTSIGLVLTGVSAVPNPVLDAGARYNYIGKVNTVKNVRSGELS VGR 171
        :|||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Db      277 TQNAHQSNISRRVGLGIACVGDFITPKLTDGTGRYHYWGRLNTR-FKTHEASLGR 335
        :|||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Qy      172 VKF 174
        :|
Db      336 YRF 338
        :|

RESULT 6
S16612
O:protein opae precursor - Neisseria gonorrhoeae (strain MS11) (fragment)
C:Species: Neisseria gonorrhoeae
A:Variety: strain MS11
C>Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997
C:Accession: S16612
R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A., A.
Mol. Microbiol. 5, 1989-1901, 1991
A>Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded
A:Reference number: S16610; MUID:92114767; PMID:1815562
A:Accession: S16612
A:Molecule type: DNA
A:Residues: 1-258 <BHA>
A:Cross-references: EMBL:X52369
A:Experimental source: strain MS11, variant 4.8
A>Note: the authors did not translate the sequence for the signal peptide
A>Note: expression of opacity proteins is regulated by the number of translate
of repeats place the start codon in frame with the rest of the protein
C:Genetics:
A:Gene: opaE
C:Superfamily: opacity protein
C:Keywords: cell surface component; transmembrane protein
F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>
F:24-258/Product: opacity protein opaE #status predicted <MAT>
F:34-42/Domain: transmembrane #status predicted <TM1>
F:43-74/Domain: extracellular #status predicted <EXT1>
F:50-60/Region: semivariable region
F:75-83/Domain: transmembrane #status predicted <TM2>
F:88-94/Domain: transmembrane #status predicted <TM3>
F:95-131/Domain: extracellular #status predicted <EXT2>
F:101-125/Region: hypervariable region HV1
F:132-146/Domain: transmembrane #status predicted <TM4>
F:152-162/Domain: transmembrane #status predicted <TM5>
F:163-209/Domain: extracellular #status predicted <EXT3>
F:210-215/Region: hypervariable region HV2
F:216-222/Domain: transmembrane #status predicted <TM6>
F:226-234/Domain: transmembrane #status predicted <TM7>
F:235-249/Domain: extracellular #status predicted <EXT4>
F:250-258/Domain: transmembrane #status predicted <TM8>

Query Match          27.8%; Score 241; DB 2; Length 258;
Best Local Similarity 29.7%; Pred.No. 4,7e-14;
Matches       76; Conservative    26; Mismatches    68; Indels     86; Gaps     10

Qy      2 KKALATIALPALPAALAEG---ASGFYVQADAHA-----KASSSLGSAK----- 44
        |||||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Db      6 KKPSSLFSSLLFSSAAQAAGSDHGKGPVQADLAYAYEHITHDYPEPTGKKDKISTVSD 65
        :||::|||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Qy      45 -----GFSFRISAGRYINDLRPADVTRYK--NYKAPSTDFFK----- 79
        :||::|||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Db      66 YFNIRTHSIHPRVSVGDFCGWRIAADYARYRWKNDKNYSVDIKELENKNQKRDLTKE 125
        :||::|||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Qy      80 -----LYSICASAIYDFTQSPVKPYLGARLSLN--RASVD-----LGG- 116
        :||::|||   |||||   |||||   |||||   |||||   |||||   |||||   |||||
Db      126 NOENGTFTHAVSLGLSAIVDFKLNDKFPIGARVAVGHVRSIDSTKTKTTEVTTLHGP 185
        :||::|||   |||||   |||||   |||||   |||||   |||||   |||||   |||||

```

F;228-236/Domain:	transmembrane #status predicted <TM7>
F;237-251/Domain:	extracellular #status predicted <EXT4>
F;252-260/Domain:	transmembrane #status predicted <TM8>

  

Query Match	27.8%; Score 241; DB 1; Length 260;
Best Local Similarity	28.8%; Pred.No. 4.7e-14;
Matches	72; Conservative 30; Mismatches 64; Indels 84; Gaps 9;

  

QY	6	ATLIALPAALAEAGSGFYVQADAAHA-----KASSLSGSAKGFS-----	47
	:	:	:
Db	14	SSLFFSAAQAASEGGRGPVQADLAYAYEHITHDPKPDPSPKGIKISTVSDFRNIRT	73
	:	:	:
QY	48	----PRISAGYRINDLARFVDVTRY-----KNYKAPSTD--	77
	:	:	:
Db	74	HSHIPRVGVDPGGWRIRIADARYARKWSDNKYSIKMWRVHKHNSRKALKTENQENG	133
	:	:	:
QY	78	--FKLYSIGASAIYDFTQSPVKPYLGARLSLN--RASVD-----LGG-	116
	:	:	:
Db	134	SFAVSSGLSALIYDQINDKPKPYIGARVAVGHVRHSIDSTKKITCLLTPTPGIMSGV	193
	:	:	:
QY	117	-----SDSFQTSIGLVLTGSYVATPNVDLDAGRYNYIGKVIVTKNVRSG	164
	:	:	:
Db	194	YKVLRTPGAHRSDSI--VGLGVIAVGFDITPKLTLDAGRYHNWGRLNTR-FKTH	250
	:	:	:
QY	165	ELSVGVVRVKF	174
	:	:	:
Db	251	EASLGVRYRF	260
	:	:	:

  

RESULT 8

S36343

opacity protein opa57 - Neisseria gonorrhoeae (strain MS11) (fragment)

N/Alternate names: outer membrane protein opa57

C/Species: Neisseria gonorrhoeae

A/Variety: strain MS11

C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C/Accession: S36343; S28626

R/Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.

EMBO J. 12, 641-650, 1993

A>Title: Variable opacity (Opa) outer membrane proteins account for the cell tr

A/Reference number: S36328; PMID:93178439; PMID:8440254

A/Accession: S36343

A/Molecule type: DNA

A/Residues: 1-237 <U>

A/Cross-references: UNIPROT:Q04880; EMBL:Z18935; NID:g49331; PIDN:CNA79368.1; P

A/Experimental source: strain MS11, variant F3

A/Note: expression of opacity proteins is regulated by the number of translated o of repeats place the start codon in frame with the rest of the protein

C/Genetics:

A/Gene: opa57

C/Superfamily: opacity protein

C/Keywords: cell surface component; transmembrane protein

F;1-237/Product: opacity protein opa57 #status predicted <MAT>

F;11-19/Domain: transmembrane #status predicted <TM1>

F;20-51/Domain: extracellular #status predicted <EXT1>

F;28-37/Region: semivariable region

F;52-60/Domain: transmembrane #status predicted <TM2>

F;65-71/Domain: transmembrane #status predicted <TM3>

F;72-110/Domain: extracellular #status predicted <EXT2>

F;78-105/Region: hypervariable region HV1

F;111-125/Domain: transmembrane #status predicted <TM4>

F;131-141/Domain: transmembrane #status predicted <TM5>

F;142-188/Domain: extracellular #status predicted <EXT3>

F;147-194/Region: hypervariable region HV2

F;189-201/Domain: transmembrane #status predicted <TM6>

F;205-213/Domain: transmembrane #status predicted <EXT4>

F;214-228/Domain: extracellular #status predicted <EXT4>

F;229-237/Domain: transmembrane #status predicted <TM8>

  

Query Match	27.7%; Score 240.5; DB 2; Length 237;
Best Local Similarity	29.6%; Pred.No. 4.7e-14;
Matches	71; Conservative 26; Mismatches 58; Indels 85; Gaps 9;

QY 17 ALAEGASGYVQADAHA-----KASSSLGS-----AKGSPRISAGY 54  
 Db 1 ASEDGGRGYPVQADLAYAYEHITHDYPEPTAPNKKNKISTVDFRNIRTRSVHPRVSGY 60  
 QY 55 RINDLREAVDYTRYKNY-----KAPSTDYK-----LYSIGAS 86  
 Db 61 DFGWRIADYARYRKNNKYSVSIKELLRNKNGNRTDLKAENQNGTTHAVSSLSLS 120  
 QY 87 AIYDFDTPSPKPYLGARLSLN--RASVD-----LGG----- 116  
 Db 121 AVYDFKLDKPKPYIGARVAYGHVRHSIDSTKTKTEVTTLHGPGTTPVYVPGKNTQDAH 180  
 QY 117 --SDSFSQTSIGLVLTGVSVAVTNVDLDAGRYNYIGKUNTVKNRSGELSVGRVKF 174  
 Db 181 RESDSIRR--VGLGAVAGVGIDITPNLTLDAGRYHYWGRLENTR-FKTHEASLGVRVRF 237

RESULT 9  
 SI6614  
 opacity protein opaF precursor - Neisseria gonorrhoeae (strain MS11) (fragments)  
 C:Species: Neisseria gonorrhoeae  
 A:Variety: strain MS11  
 C:Date: 04-Jun-1997 #sequence\_revision 17-Oct-1997 #text\_change 17-Oct-1997  
 C:Accession: SI6614  
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I.  
 Mol. Microbiol. 5, 1889-1901, 1991  
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein  
 A:Reference number: SI6610; MUID:92114767; PMID:1815562  
 A:Accession: SI6614  
 A:Molecule type: DNA  
 A:Residues: 1-257 <BHA>  
 A:Cross-references: EMBL:X52368  
 A:Experimental source: strain MS11, variant 4.8  
 A:Note: the authors did not translate the sequence for the signal peptide  
 A:Note: the authors did not translate the sequence for the signal peptide  
 A:Note: expression of opacity proteins is regulated by the number of translated repeat e  
 of repeats place the start codon in frame with the rest of the protein  
 C:Genetics:  
 A:Gene: opaF  
 C:Superfamily: opacity protein  
 C:Keywords: cell surface component; transmembrane protein  
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
 F:24-42/Domain: transmembrane #status predicted <WAT>  
 F:34-42/Domain: transmembrane #status predicted <WAT>  
 F:43-74/Domain: extracellular #status predicted <EXT1>  
 F:51-60/Region: semivariable region  
 F:75-83/Domain: transmembrane #status predicted <TM2>  
 F:88-94/Domain: transmembrane #status predicted <TM3>  
 F:95-131/Domain: extracellular #status predicted <EXT2>  
 F:101-126/Region: hypervariable region HV1  
 F:132-146/Domain: transmembrane #status predicted <TM4>  
 F:152-162/Domain: transmembrane #status predicted <TM5>  
 F:163-208/Domain: extracellular #status predicted <EXT3>  
 F:168-214/Region: hypervariable region HV2  
 F:209-221/Domain: transmembrane #status predicted <TM6>  
 F:225-233/Domain: transmembrane #status predicted <TM7>  
 F:234-248/Domain: extracellular #status predicted <EXT4>  
 F:249-257/Domain: transmembrane #status predicted <TM8>

Query Match 27.7%; Score 240.5; DB 2; Length 257;  
 Best Local Similarity 29.2%; Pred. No. 5.2e-14;  
 Matches 74; Conservative 26; Mismatches 72; Indels 81; Gaps 9;

QY 2 KKALATLIALAPAAALAE-----ASGFYVQADAHA-----KASSSLGS- 44  
 Db 6 KKPSLLFSSLLFSSAAQAAGEHGRGYPVQADLAYAYEHITHDYPEPTGKKDKISTVSD 65  
 QY 45 -----GFSPRISAGRYINDLRFAVDYTRYK--NYKAPSTDYK----- 79  
 Db 66 YFRNIRTHSIHPRVSVGYDFGWRIAADYARYRKWNKNKYSVDIKELENKQNKRDLDKTE 125  
 QY 80 -----LYSIGASAIYDFDTPSPKPYLGARLSLN--RASVD-----LGG 116

Db 126 NOENGTTHAVSSLSLSAVYDFKLDKPKPYIGARVAYGHVRHSIDSTKTKTKFLTSSVG 185  
 QY 117 -----SDSFSQTSIGLVLTGVSVAVTNVDLDAGRYNYIGKUNTVKNV 161  
 Db 186 LNPVTYVTEENTQNAHQSNIRRVGLGIAGVGPDITPKLTLDGTRYHYWGRLENTR-F 244  
 QY 162 RSGELSVGRVKF 174  
 Db 245 KTHEASLGVRVRF 257

RESULT 10  
 SI6616  
 opacity protein opaD precursor - Neisseria gonorrhoeae (strain MS11) (fragments)  
 C:Species: Neisseria gonorrhoeae  
 A:Variety: strain MS11  
 C:Date: 04-Jun-1997 #sequence\_revision 17-Oct-1997 #text\_change 17-Oct-1997  
 C:Accession: SI6616  
 R:Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I.  
 Mol. Microbiol. 5, 1889-1901, 1991  
 A:Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a family of repeats place the start codon in frame with the rest of the protein  
 A:Reference number: SI6610; MUID:92114767; PMID:1815562  
 A:Accession: SI6616  
 A:Molecule type: DNA  
 A:Residues: 1-266 <BHA>  
 A:Cross-references: EMBL:X52372  
 A:Experimental source: strain MS11, variant 4.8  
 A:Note: the authors did not translate the sequence for the signal peptide  
 A:Note: expression of opacity proteins is regulated by the number of translated repeat e  
 of repeats place the start codon in frame with the rest of the protein  
 C:Genetics:  
 A:Gene: opaD  
 C:Superfamily: opacity protein  
 C:Keywords: cell surface component; transmembrane protein  
 F:1-10,11-23/Domain: signal sequence (fragments) #status predicted <SIG>  
 F:24-266/Product: opacity protein opaD #status predicted <WAT>  
 F:34-42/Domain: transmembrane #status predicted <TM1>  
 F:43-74/Domain: extracellular #status predicted <EXT1>  
 F:51-60/Region: semivariable region  
 F:75-83/Domain: transmembrane #status predicted <TM2>  
 F:88-94/Domain: transmembrane #status predicted <TM3>  
 F:95-139/Domain: extracellular #status predicted <EXT2>  
 F:101-134/Region: hypervariable region HV1  
 F:140-154/Domain: transmembrane #status predicted <TM4>  
 F:160-170/Domain: transmembrane #status predicted <TM5>  
 F:171-217/Domain: extracellular #status predicted <EXT3>  
 F:176-223/Region: hypervariable region HV2  
 F:218-230/Domain: transmembrane #status predicted <TM6>  
 F:234-242/Domain: transmembrane #status predicted <TM7>  
 F:243-257/Domain: extracellular #status predicted <EXT4>  
 F:258-266/Domain: transmembrane #status predicted <TM8>

Query Match 27.5%; Score 239; DB 2; Length 266;  
 Best Local Similarity 29.0%; Pred. No. 7.3e-14;  
 Matches 76; Conservative 26; Mismatches 70; Indels 90; Gaps 8;

QY 2 KKALATLIALAPAAALAE-----ASGFYVQADAHA-----KASSSLGS- 42  
 Db 6 KKPSLLFSSLLFSSAAQAAGEHGRGYPVQADLAYAYEHITHDYPEPTGKQAQLSTVSD 65  
 QY 43 -----AKGFSPRISAGRYINDLRFAVDYTRYK----- 69  
 Db 66 YFRNIRTHSIHPRVSVGYDFGWRIAADYARYRKWNKNKYSVNIKELLRNNDNANSGSHL 125  
 QY 70 NYKAPSTDYK-----LYSIGASAIYDFDTPSPKPYLGARLSL----- 107  
 Db 126 NIKTRKTHRENGTTHAASSLSGLSAVDYDFDTPSPKPYIGRVAHYGHVHQRVRSVQQETI 185  
 QY 108 -----NRASV-----DLGGSDFSQTSIGLVLTGVSVAVTNVDLDAGRYNYI 152  
 Db 186 AVTYPQNAASVVTNAPIRKLPHEHSRSISLGFAGVAGVGIDITPNLTLDAGRYHYNW 245  
 QY 153 GKUNTVKNRSGELSVGRVKF 174





Fri May 20 10:37:41 2005

S72343  
 opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)  
 N:Alternate names: cell invasion protein opaH  
 C:Species: Neisseria gonorrhoeae  
 A:Variety: isolate 15063G  
 C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C:Accession: S72343  
 R:Waldbeser, L.S.; Ajioke, R.S.; Merz, A.J.; Puaoli, D.; Lin, L.; Thomas, M.; So, M.  
 Mol. Microbiol. 13, 919-928, 1994  
 A:title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in  
 A:Reference number: S72343; MUID:95115561; PMID:7815949  
 A:Accession: S72343  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-283 <WAL>  
 A:Cross-references: UNIPROT:Q50943; EMBL:U13708; NID:G535357; PIDN:AAA74082.1; PID:G5353  
 A:Experimental source: isolate 15063G  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
 A:Note: expression of opacity proteins is regulated by the number of translated repeat e  
 of repeats place the start codon in frame with the rest of the protein  
 C:Superfamily: opacity protein  
 C:Keywords: cell surface component; transmembrane protein  
 F:1-48/Domain: signal sequence #status predicted <SIG>  
 F:49-263/Product: opacity protein opaH #status predicted <MAT>  
 F:58-66/Domain: transmembrane #status predicted <TM1>  
 F:67-98/Domain: extracellular #status predicted <EXT1>  
 F:75-84/Region: semivariable region  
 F:99-107/Domain: transmembrane #status predicted <TM2>  
 F:112-118/Domain: transmembrane #status predicted <TM3>  
 F:119-155/Domain: extracellular #status predicted <EXT2>  
 F:125-150/Region: hypervariable region HV1  
 F:156-170/Domain: transmembrane #status predicted <TM4>  
 F:176-186/Domain: transmembrane #status predicted <TM5>  
 F:187-234/Domain: extracellular #status predicted <EXT3>  
 F:192-240/Region: hypervariable region HV2  
 F:235-247/Domain: transmembrane #status predicted <TM6>  
 F:251-259/Domain: transmembrane #status predicted <TM7>  
 F:260-274/Domain: extracellular #status predicted <EXT4>  
 F:275-283/Domain: transmembrane #status predicted <TM8>

Query Match 27.2%; Score 236; DB 2; Length 283;  
 Best Local Similarity 27.9%; Pred. No. 1.5e-13;  
 Matches 68; Conservative 29; Mismatches 67; Indels 80; Gaps 7;

QY	10	ALALPAALAEAGSGFYQDAAHAKA-----SSSLGSAGK-----FS 47
DB	41	SLLSAAQAASEAMRGYPYQADLFAAEKITHDYPEPTGKGTISTVSDYFRNIRTHSVH 100
QY	48	PRISAGYRINDLRFADVITYKNY-----KAPS-----TDPKLY 81
DB	101	PRVSVGYDFGGWRIAADYARYKWNKNYSVNIERVQEAHSNRIDLKAEQNGTFHVS 160
QY	82	STGASAIYDFDTQSPVKYLGARLSN--RASVDL----- 114
DB	161	SIGLSAVYDFKLNDRKFPYIGARVAYGHVRHSIDSTKTKILTSTFYGVATKPTYDIGP 220
QY	115	-----CGSDSFSQTSIGLVLTGVSVAVTPNVLDLAGYRNYIGKVTYKVNRSGLSVGV 170
DB	221	KTQDAHQESNSIRRVGLGVGIAGVGFDITPKLTDLTGYHYWGRLENTF-PKTHEASLGM 279
QY	171	RVKF 174
DB	280	RYRF 283

Search completed: May 19, 2005, 21:02:19  
 Job time : 70 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2005, 20:24:55 ; Search time 357 Seconds  
(without alignments)  
249.585 Million cell updates/sec

Title: US-10-650-123-2

Perfect score: 868

Sequence: 1 MKKALATLIALPAAALAE.....VNTVNVRSGLSVGVKVF 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	868	100.0	174	2	P96943	P96943 neisseria m
2	864	99.5	174	2	Q7DDM2	Q7ddm2 neisseria m
3	864	99.5	174	2	Q9RP17	Q9rp17 neisseria m
4	857	98.7	174	2	Q9R2R1	Q9r2r1 neisseria m
5	854	98.4	174	2	P95372	P95372 neisseria m
6	854	98.4	174	2	Q7AR60	Q7ar60 neisseria m
7	852	98.2	174	2	Q9RP16	Q9rp16 neisseria m
8	846	97.5	174	2	Q9RP18	Q9rp18 neisseria m
9	825	95.0	174	2	P95343	P95343 neisseria g
10	824.5	95.0	175	2	P95371	P95371 neisseria m
11	303.5	35.0	177	2	Q65RV6	Q65rv6 manheimia
12	256	23.5	226	2	Q85TE2	Q85te2 manheimia
13	247	28.5	256	2	Q51124	Q51124 neisseria m
14	246.5	28.4	186	2	Q9CM19	Q9cm19 pasteurella
15	244	28.1	234	2	O07280	O07280 neisseria m
16	244	28.1	234	2	Q9R7I9	Q9r7i9 neisseria m
17	243	28.0	234	2	Q9R7I8	Q9r7i8 neisseria m
18	241.5	27.8	232	2	Q9K4T9	Q9k4t9 neisseria l
19	241.5	27.8	241	2	Q9AE80	Q9ae80 neisseria m
20	240.5	27.7	230	2	Q9R9A7	Q9r9a7 neisseria m
21	240.5	27.7	237	1	OPAK_NEIGO	Q04880 neisseria g
22	240	27.6	241	2	Q9K4T4	Q9k4t4 neisseria l
23	240	27.6	256	2	Q51126	Q51126 neisseria m
24	240	27.6	259	2	Q51125	Q51125 neisseria m
25	239.5	27.6	232	2	Q9R3P5	Q9r3p5 neisseria m
26	239	27.5	260	1	OPR1_NEIMC	P10170 neisseria m
27	238.5	27.5	257	2	Q50929	Q50929 neisseria f
28	238	27.4	234	2	O07287	O07287 neisseria m
29	238	27.4	237	2	O31176	O31176 neisseria m
30	237	27.3	239	2	Q7BW15	Q7bw15 neisseria m
31	237	27.3	262	2	O33388	O33388 neisseria m

## RESULT 1

P96943	PRELIMINARY;	PRT;	174 AA.
ID	P96943		
AC	P96943;		
DT	01-MAY-1997 (TrEMBLrel. 03, Created)		
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Outer membrane protein precursor (Surface protein A).		
GN	Name=nsa;		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=608B;		
RX	MEDLINE=97258610; PubMed=9104804;		
RA	Martin D., Cadieux N., Hamel J., Brodeur B.R.;		
RT	"Highly conserved Neisseria meningitidis surface protein confers		
RT	protection against experimental infection.";		
RL	J. Exp. Med. 185:1173-1183(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=608B;		
RX	MEDLINE=99270944; PubMed=10338491;		
RA	Plante M., Cadieux N., Rioux C.R., Hamel J., Brodeur B.R.; Martin D.;		
RT	"Antigenic and molecular conservation of the gonococcal NspA		
RT	protein.";		
RL	Infect. Immun. 67:2855-2861(1999).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=608B;		
RX	MEDLINE=99386904; PubMed=10456958;		
RA	Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R.; Martin D.;		
RT	"Bactericidal and cross-protective activities of a monoclonal antibody		
RT	directed against Neisseria meningitidis NspA outer membrane protein.";		
RL	Infect. Immun. 67:4955-4959(1999).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[6]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[7]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[8]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[9]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[10]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[11]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[12]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[13]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[14]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[15]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[16]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[17]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[18]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[19]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[20]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[21]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[22]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[23]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[24]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[25]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[26]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[27]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[28]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[29]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[30]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[31]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[32]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[33]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[34]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[35]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[36]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[37]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[38]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[39]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[40]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[41]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[42]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[43]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[44]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[45]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[46]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[47]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[48]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[49]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect. Immun. 0:0-0(1999).		
RN	[50]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=M986, NG6/88, and NGP165;		
RA	Moe G.R., Tan S., Granoff D.M.;		
RT	"Differences in Surface Expression of Neisserial Surface Protein A		
RT	among Neisseria meningitidis Group B strains.";		
RL	Infect.		

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FT SIGNAL 1 19 Potential.
SQ SEQUENCE 174 AA; 18425 MW; E8B02767DDC6FE19 CRC64;

Query Match 100.0%; Score 868; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e-69;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFTKLYSGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFTKLYSGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGLGLVLTGVSAYATPNVDLDAGYRNYIKVNTVKNVRSGLSGELSGVRVKF 174
DB 121 SQTSLGLGLVLTGVSAYATPNVDLDAGYRNYIKVNTVKNVRSGLSGELSGVRVKF 174

RESULT 2
Q7DDM2 PRELIMINARY; PRT; 174 AA.
ID Q7DDM2
AC Q7DDM2; 2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Outer membrane protein NsgA.
GN OrderedLocusNames=NM0663;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Clifton H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qian H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815 (2000).
DR EMBL; AE002420; AAF41081.1; -.
DR TIGR; NMB0663; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Complete proteome.
SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;
Best Local Similarity 99.4%; Pred. No. 3.3e-69;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFTKLYSGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFTKLYSGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGLGLVLTGVSAYATPNVDLDAGYRNYIKVNTVKNVRSGLSGELSGVRVKF 174
DB 121 SQTSLGLGLVLTGVSAYATPNVDLDAGYRNYIKVNTVKNVRSGLSGELSGVRVKF 174

RESULT 3
Q9RP17 PRELIMINARY; PRT; 174 AA.
ID Q9RP17
AC Q9RP17;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Surface protein A.
GN Name=nsa;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CU385;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0 (1999).
DR EMBL; AF175678; AAD53281.1; -.
DR PIR; G81174; G81174.
DR PDB; 1P4T; X-ray; A=20-174.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18397 MW; E8B02767DDC6E109 CRC64;

Query Match 99.5%; Score 864; DB 2; Length 174;
Best Local Similarity 99.4%; Pred. No. 3.3e-69;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFTKLYSGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120
DB 61 FAVDYTRYKNYKAPSTDFTKLYSGASAIYDFDTQSPVKPYLGARLSLNRAVDLGGSDSF 120

QY 121 SQTSLGLGLVLTGVSAYATPNVDLDAGYRNYIKVNTVKNVRSGLSGELSGVRVKF 174
DB 121 SQTSLGLGLVLTGVSAYATPNVDLDAGYRNYIKVNTVKNVRSGLSGELSGVRVKF 174

RESULT 4
Q9R2R1 PRELIMINARY; PRT; 174 AA.
ID Q9R2R1
AC Q9R2R1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Surface protein A.
GN Name=nsa;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M136, and BZ232;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0 (1999).
DR EMBL; AF175679; AAD53282.1; -.
DR EMBL; AF175677; AAD53280.1; -.
DR HSP; Q9RP17; 1P4T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.

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DR InterPro: IPR003394; Porin_opacity.
DR Pfam: PF02462; Opacity; 1.
SQ SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;

Query Match
Best Local Similarity 98.7%; Score 857; DB 2; Length 174;
Matches 171; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

QY 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174
Db 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174

RESULT 5
P95372 PRELIMINARY; PRT; 174 AA.
AC P95372;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Outer membrane protein precursor.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z4063;
RX MEDLINE=99386904; PubMed=10456958;
RA Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
RT "Bactericidal and cross-protective activities of a monoclonal antibody
RT directed against Neisseria meningitidis NspA outer membrane protein.";
RL Infect. Immun. 67:4955-4959 (1999).
DR EMBL: U52068; AAB41580.1; -.
DR FIR; B81932; B81932.
DR HSP; Q9RP17; 1P4T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro: IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match
Best Local Similarity 98.4%; Score 854; DB 2; Length 174;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

QY 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174
Db 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174

RESULT 6
Q7AR60 PRELIMINARY; PRT; 174 AA.
ID Q7AR60
AC Q7AR60;

Query Match
Best Local Similarity 98.4%; Score 854; DB 2; Length 174;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

QY 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174
Db 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174

RESULT 7
Q9RP16 PRELIMINARY; PRT; 174 AA.
ID Q9RP16
AC Q9RP16;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Surface protein A.
GN Name=nsrA;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
RT among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0 (1999).
DR EMBL; AF175681; AAD53284.1; -.
DR HSP; Q9RP17; 1P4T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro: IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
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DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Outer membrane protein.
GN Name=nsrA; OrderedLocusNames=NMA0862;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=2222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman G., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagals K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506 (2000).
DR EMBL; AL162754; CAB84143.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro: IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
KW Complete proteome.
SQ SEQUENCE 174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;

Query Match
Best Local Similarity 98.4%; Score 854; DB 2; Length 174;
Matches 171; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
Db 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60

QY 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRAVDLGSDSF 120

QY 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174
Db 121 SQTSLGLVLTGVSVAVTNPVNDLDAGRYNYIGKNTVKNVRSGBLSVGVVRVKF 174

RESULT 7
Q9RP16 PRELIMINARY; PRT; 174 AA.
ID Q9RP16
AC Q9RP16;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Surface protein A.
GN Name=nsrA;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88;
RA Moe G.R., Tan S., Granoff D.M.;
RT "Differences in Surface Expression of Neisserial Surface Protein A
RT among Neisseria meningitidis Group B strains.";
RL Infect. Immun. 0:0-0 (1999).
DR EMBL; AF175681; AAD53284.1; -.
DR HSP; Q9RP17; 1P4T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro: IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
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Query Match      95.0%; Score 824.5; DB 2; Length 175;
Best Local Similarity 95.4%; Pred. No. 1.1e-65;
Matches 167; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
   |||||
DB 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 60
   |||||

QY 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDS 119
   |||||
DB 61 FAVDYTRYKNYKQVSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDLGGSDS 120
   |||||

QY 120 FQSTSGILGVLTVSYATPNVDLDAGYRNYIGKNTVKNVRSGLSGVGRVKF 174
   |||||
DB 121 FQSTSGILGVLTVSYATPNVDLDAGYRNYIGKNTVKNVRSGLSGVGRVKF 175
   |||||

RESULT 11
Q5SRV6 PRELIMINARY; PRT; 177 AA.
AC Q65RV6;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=MS1697;
OS Mannheimia succiniciproducens MBEL55E.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 0:0-0(2004).
DR EMBL; AE016827; AAU38304.1; -.
KW Hypothetical protein.
SQ SEQUENCE 177 AA; 18969 MW; B6ACFOAA75915B57 CRC64;

Query Match      35.0%; Score 303.5; DB 2; Length 177;
Best Local Similarity 40.2%; Pred. No. 3.8e-19;
Matches 74; Conservative 25; Mismatches 68; Indels 17; Gaps 6;

QY 1 MKKALATLIALPAAALAEAGSGFYVQADAAHAKASSLSGSAKGFSPRISAGYRINDLR 59
   |||||
DB 1 MKKTLTALIAALWVSAQA-----NYYVEGNAGYSKIKSGEVSDHRFSPNALGYDTGDM 56
   |||||

QY 60 RFADVTRYKNYKAPSTDFKLYSIGASAIYDFTQSPVKPYLGARLSLNRAVDL----- 114
   |||||
DB 57 RYADYTHYKSTDCNSENKAGHGFVSAIYDIEVSPVKPYLGARLSAN--DIDAKEKR 114
   |||||

QY 115 -GGSDFSQT---STGLGLTVGVSVAFTPNVDLDAGYRNYIGKNTVKNVRSGLSGV 170
   |||||
DB 115 SCSRIKETDSYKLYGALAGVQVQAKVDSLNGGVNRLGKANG-HNINQYAKVGV 173
   |||||

QY 171 RVKF 174
DB 174 RYDF 177

RESULT 12
Q5STE2 PRELIMINARY; PRT; 226 AA.
AC Q65TE2;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=MS1161;

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OS Mannheimia succiniciproducens MBEL55E.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP SEQUENCE FROM N.A.
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 0:0-0(2004).
DR EMBL; AE016827; AAU37768.1; -.
KW Hypothetical protein.
SQ SEQUENCE 226 AA; 25460 MW; 106C558F9B4C1504 CRC64;

Query Match      29.5%; Score 256; DB 2; Length 226;
Best Local Similarity 35.1%; Pred. No. 8.6e-15;
Matches 72; Conservative 26; Mismatches 67; Indels 40; Gaps 8;

QY 1 MKKALATLIALPAAALAEAGS-GFYVQADAAHAKASSLSGSAKG-----FSPR 49
   |||||
DB 31 MKK---TTLAVAIGILAISSASANWYVQGVGVSKIKAS-----GMDLDFKONVFPQR 82
   |||||

QY 50 ISAGYRINDLRFAVDYTRYKNYK-----APSTDFKLYSIGASAIYDFTQSP 96
   |||||
DB 83 ISAGYDFGDIRLAVDYSHIGAKDHYTLFRGEQWETSGTSTVETNSFGISAIYDFNLNTS 142
   |||||

QY 97 VKPYLGARLSLNRAV-----DLGSSDSFSQ--TSIGLGLTVGVSVAFTPNVDLDAGYR 149
   |||||
DB 143 LMPYVGVRLSENLSLKFDHWRDNASSEYSSTKTKFYGALAGVQVYHLTDLNLLNVGVEY 202
   |||||

QY 150 NYICKVNTVKNVRSGLSGVGRVKF 174
DB 203 NRLGKVEVK-IHQYSKAGLRVNF 226

RESULT 13
Q51124 PRELIMINARY; PRT; 256 AA.
AC Q51124;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Opacity outer membrane protein (Fragment).
GN Name=opa;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=24197;
RX MEDLINE=98129089; PubMed=9467908;
RA Hobbs M.M., Malorny B., Prasad P., Morelli G., Kusecek B.,
RA Heckels J.E., Cannon J.G., Achtman M.;
RT "Recombinational reassortment among opa genes from ET-37 complex
RT Neisseria meningitidis isolates of diverse geographical origins.";
RL Microbiology 144:157-166(1998).
DR EMBL; U37255; AAC46101.1; -.
DR FIR; B60119; B60119.
DR FIR; S77737; S77737.
DR HSSP; Q9RP17; 1P4T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015288; F:porin activity; IEA.
DR InterPro; IPR003394; Porin_opacity.
DR Pfam; PF02462; Opacity; 1.
FT NON TER 1
SQ SEQUENCE 256 AA; 28335 MW; 9D41C6079C6DD13F CRC64;

Query Match      28.5%; Score 247; DB 2; Length 256;
Best Local Similarity 28.3%; Pred. No. 6.3e-14;
Matches 69; Conservative 33; Mismatches 64; Indels 78; Gaps 7;

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